

STIC-Biotech/ChemLib

75876

From: Chan, Christina
Sent: Tuesday, September 17, 2002 8:22 AM
To: Kemmerer, Elizabeth; STIC-Biotech/ChemLib
Subject: RE: rush seq search req

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE, 1644
CM 1, Room 9B19
308-3973

-----Original Message-----

From: Kemmerer, Elizabeth
Sent: Tuesday, September 17, 2002 8:21 AM
To: Chan, Christina
Subject: rush seq search req

Chris-

Please approve the following rush request for a date case that Bonnie just transferred to me.
Thanks.

STIC:

Please rush a search of SEQ ID NO: 69 for 09/944396. Thanks.

Elizabeth (Betsy) Kemmerer
Art Unit 1646
308-2673
CM1-10B17
Mailbox: 10D19

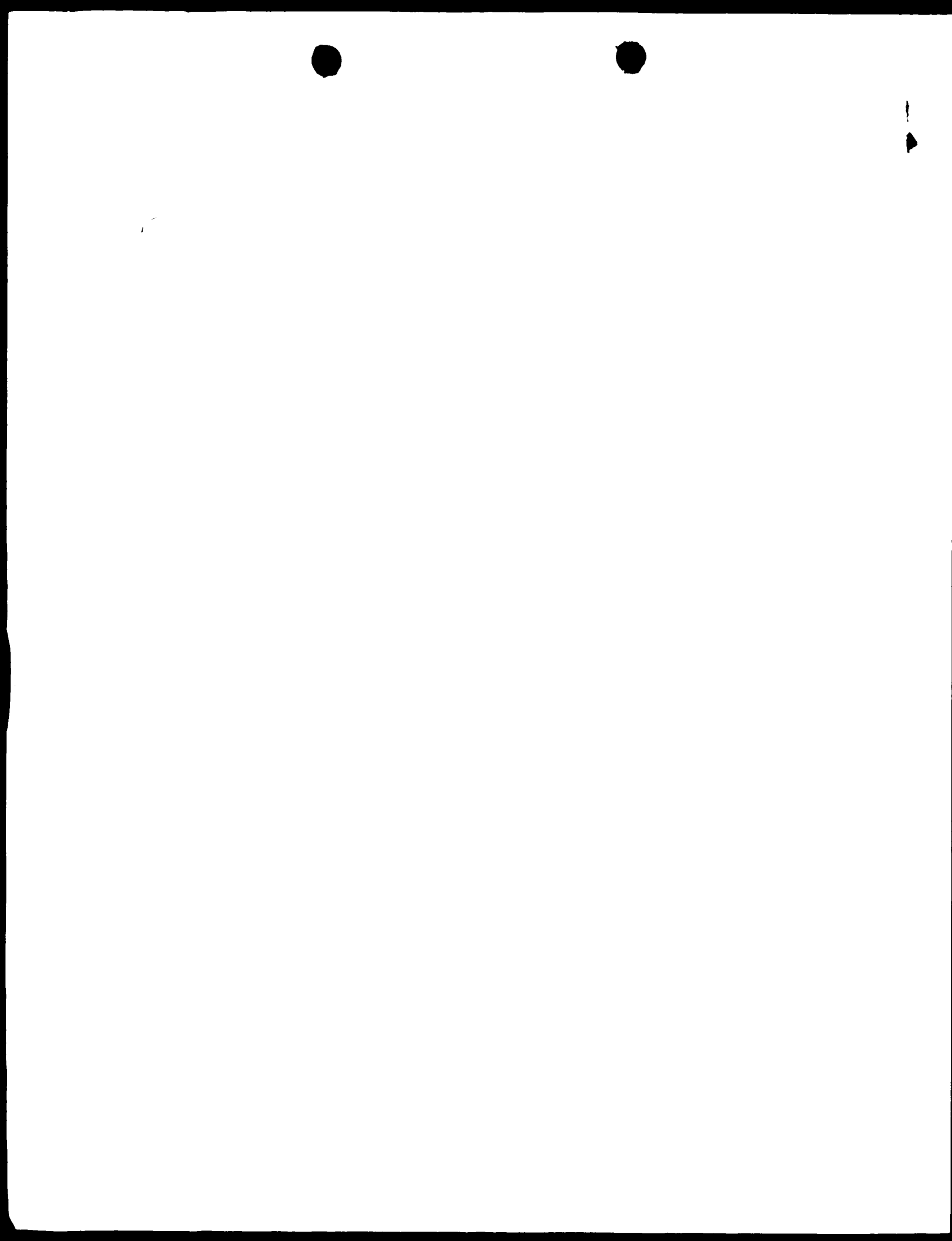
Searcher: P. Schreiber
Phone: 308-4272
Location: CM1 6A03
Date Picked Up: 9/17
Date Completed: 9/18
Searcher Prep/Review: 8
Clerical: _____
Online time: 5

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: CompuLink
WWW/Internet: _____
Other (specify): _____



Query Match 100.0%; Score 3135; DB 21; Length 598;
 Best Local Similarity 100.0%; Pred. No. 26-191;
 Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPALLLALGPGVQVSGVQSGQSQPQVFCFLAQGCTVPRDVPVDTWGLYVF 60
 DB 1 mcsrvplllpalllalgpgvqvsqvsqqsqpsqlvtctarqvtprdpvdyqlvyve 60

QY 61 ENGITMLDASSFACIPGCIQLLULSQNLASLRLPRLILLDLSSLSLALRPGILLDTANVE 120
 DB 61 engitmlsdassfaclpfcilqlululsqnlaslrlprrllldlsslsllalepdlldtanve 120

QY 121 ALRLACIGLQCTDFPFI FSPFNLHMDVSNQGLRVPVWIPFGLRGLRLRLAGNTRIAQL 180
 DB 121 alrlaciglcqctdfpfi fspfnlhmdvsnqglrvpvpwipfglrqlrlrlagntriaql 180

QY 181 RPNRLACIAAI QPI DVSNLSIGALPGNSGLFPPLRLILAAAPNPNCVPSWGPVWRE 240
 DB 181 rpnrlaciaaai qpi dvsnlsigalpgnsglfpplrlilaaapnpncvpswgpvwre 240

QY 241 SHVTLASPETHCHFPKKNAGRELLELYADRGCHAI RTAIVPTIRPVVREPTALSSSL 300
 DB 241 shvtlaspethchfpkknagrellelyadrgchaitaivptirpvvrepthalsssl 300

QY 301 APTWLSPTAPATAPSPSTAPPTVPVPGQCHPSPTLNATGCHGTPPHLAWLPAPG 360
 DB 301 aptwlsptapatapspstapptvpvpqchpsptlnatgchgtpphlawlpapg 360

QY 361 FTGLYCSQMGCTPSPPTVPVPRPERSI FLCTPVSQTSI PVGLQVLYGSSVWLSLP 420
 DB 361 ftglycsqmgctpsspptvpvprrpersi flctpvsqtsi pvglqvlygssvwlslp 420

QY 421 LTYRNLSGPKKVLRLPASLAETVTLRPNATYSVCMPLGPGVPEGEACGEAHI 480
 DB 421 ltyrnlsgpkkvlrlpaslaetvtl rpnatysvcmplpgpgvpegeacgeahi 480

QY 481 PPAVSHNHAIVTQAREGNI PLILAPALAAVLLAAVCAAYCVRRGRAMAAADRGQV 540
 DB 481 ppaushnhaivtqaregni plilapalaaavllaaavcaaycvrrgramaaadrgqv 540

QY 541 CHCAGPLEGCKVPL FPGPKATFGGSEFALPGSGSECVPLMGCPGCPGLSPHAKPYL 598
 DB 541 chcagplegckvpl fpgpkatfggsefalpgsgsecvplmgcpgcpplshakpyl 598

RESULT 4

AA17831
 AA17831 standard; Protein; 598 AA.

AA17831;

12-AUG-1999 (first entry)

Human PKG57 protein sequence.

Human PKG protein; tumour necrosis factor family; TNF; cytokine;
 secreted protein; transmembrane protein; inflammation disorder.

Human sapiens.

W09928462-A2.

10-JUN-1999.

01-DEC-1998; 98W0-US25108.

25-FEB-1998; 98US-0075945.

04-DEC-1997; 97US-0067411

11-DEC-1997; 97US-0069278.

11-DEC-1997; 97US-0069444

11-DEC-1997; 97US-0069335.

12-FEB-1997; 97US-0069425.

PR 16-DEC-1997; 97US-0069694.
 PR 16-DEC-1997; 97US-0069696.
 PR 16-DEC-1997; 97US-0069702.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 05-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX (GENE) GENENTECH INC.
 PA Baker KP, Chen J, Goddard A, Gurney AL, Wood WL;
 P1 Yuan J;
 XX WPI; 1999-371118/31.
 DR N-PSDB; AAX80056.
 XX Nucleic acids encoding PRO secreted and transmembrane proteins
 XX Claim 12; Fig 29; 123pp; English.
 XX The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 XX Sequence 598 AA;

Query Match 99.78; Score 3126; DB 20; Length 598;

Best Local Similarity 99.8%; Pred. No. 7.66-191;

Matches 597; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPALLLALGPGVQVSGVQSGQSQPQVFCFLAQGCTVPRDVPVDTWGLYVF 60

DB 1 mcsrvplllpalllalgpgvqvsqvsqqsqpsqlvtctarqvtprdpvdyqlvyve 60

QY 61 ENGITMLDASSFACIPGCIQLLULSQNLASLRLPRLILLDLSSLSLALRPGILLDTANVE 120

DB 61 engitmlsdassfaclpfcilqlululsqnlaslrlprrllldlsslsllalepdlldtanve 120

QY 121 ALRLACIGLQCTDFPFI FSPFNLHMDVSNQGLRVPVWIPFGLRGLRLRLAGNTRIAQL 180

DB 121 alrlaciglcqctdfpfi fspfnlhmdvsnqglrvpvpwipfglrqlrlrlagntriaql 180

QY 181 RPNRLACIAAI QPI DVSNLSIGALPGNSGLFPPLRLILAAAPNPNCVPSWGPVWRE 240

DB 181 rpnrlaciaaai qpi dvsnlsigalpgnsglfpplrlilaaapnpncvpswgpvwre 240

QY 241 SHVTLASPETHCHFPKKNAGRELLELYADRGCHAI RTAIVPTIRPVVREPTALSSSL 300

DB 241 shvtlaspethchfpkknagrellelyadrgchaitaivptirpvvrepthalsssl 300

QY 301 APTWLSPTAPATAPSPSTAPPTVPVPGQCHPSPTLNATGCHGTPPHLAWLPAPG 360

DB 301 aptwlsptapatapspstapptvpvpqchpsptlnatgchgtpphlawlpapg 360

QY 361 FTGLYCSQMGCTPSPPTVPVPRPERSI FLCTPVSQTSI PVGLQVLYGSSVWLSLP 420

DB 361 ftglycsqmgctpsspptvpvprrpersi flctpvsqtsi pvglqvlygssvwlslp 420

QY 421 LTYRNLSGPKKVLRLPASLAETVTLRPNATYSVCMPLGPGVPEGEACGEAHI 480

DB 421 ltyrnlsgpkkvlrlpaslaetvtl rpnatysvcmplpgpgvpegeacgeahi 480

QY 481 PPAVSHNHAIVTQAREGNI PLILAPALAAVLLAAVCAAYCVRRGRAMAAADRGQV 540

DB 481 ppaushnhaivtqaregni plilapalaaavllaaavcaaycvrrgramaaadrgqv 540

QY 541 GPAGAPLEGVKVPLEPPKATEGGREALPPSSSECEVPMGSPGPGCLQSPPLIAKPYI 598
 DB 541 GPAGAPLEGVKVPLEPPKATEGGREALPPSSSECEVPMGSPGPGCLQSPPLIAKPYI 598

RESULT 5
 AAB07428
 ID AAB07428 standard; Protein: 673 AA.
 AC AAB07428.
 DT 20-OCT-2000 (first entry)
 XX Amino acid sequence of a leucine-rich surface glycoprotein (LRSg).
 XX Leucine-rich surface glycoprotein; LRSg.
 XX Homo sapiens.
 OS
 GN
 KI
 FT Peptide
 FT 1..23 Location/Qualifiers
 FT /note= "signal peptide"
 FT Region
 FT 77..309 /note= "leucine-rich region"
 FT Region
 FT 101..123 /note= "leucine-rich repeat"
 FT Region
 FT 125..147 /note= "leucine-rich repeat"
 FT Region
 FT 149..171 /note= "leucine-rich repeat"
 FT Region
 FT 217..238 /note= "leucine-rich repeat"
 FT Region
 FT 240..263 /note= "leucine-rich repeat"
 FT Region
 FT 289..309 /note= "leucine-rich repeat"
 FT Region
 FT 409..441 /note= "PCF-like domain"
 FT Domain
 FT 460..535 /note= "fibronectin type III domain"
 FT Domain
 FT 576..599 /note= "transmembrane domain"
 XX
 PN W0200042170 A1.
 DB 20-JUL-2000.
 XX
 XX 21-APR-1999; 99W0 0508792.
 XX
 XX 21 APR 1998; 98W0 2063950.
 XX
 PA (MILL.) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Holzman JA;
 XX
 XX WPI; 2000-422823/42.
 DR N-PSDB; AAA58765, AAA58766.
 XX
 XX New leucine-rich surface glycoprotein (LRSg) polynucleotides and
 PT polypeptides used in diagnostics and screening assays to identify
 PT modulators used to treat LRSg associated disorders -
 XX
 XX Claim 9; Fig 1; 139pp; English.
 XX
 CC The present sequence represents a leucine-rich surface glycoprotein
 CC (LRSg). Modulators of LRSg can be used to treat disorders
 CC characterized by aberrant LRSg protein or nucleic acid expression
 CC or activity. The LRSg proteins can be used to treat disorders
 CC associated with insufficient or excessive production of LRSg, or
 CC LRSg target molecules LRSg proteins and antibodies specific for
 CC it are used in screening assays, diagnostic assays, prognostic
 CC assays for monitoring clinical trials and in pharmacogenetics.

XX Sequence 673 AA;
 SQ

Query Match 98.4%; Score 3083.5; DB 21; Length 673;
 Best Local Similarity 88.7%; Pred. No. 4.4e-188;
 Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLDLLLDAALPGVQGRPSQCSQSQPVVECTARQCTTPPRVPPDVGLVYF 60
 DB 1 MCSRVPLLLDLLLDAALPGVQGRPSQCSQSQPVVECTARQCTTPPRVPPDVGLVYF 60
 QY 61 ENGHTMLDASSPAGLQCLQLLLDSQNIAS----- 90
 DB 61 ENGHTMLDASSPAGLQCLQLLLDSQNIAS----- 90
 QY 62 GASTMLDASSPAGLQCLQLLLDSQNIAS----- 120
 DB 62 GASTMLDASSPAGLQCLQLLLDSQNIAS----- 120
 QY 91 -----LRLPRLLLLLSHNS 105
 DB 91 -----LRLPRLLLLLSHNS 105
 DB 121 RQIRRIERYLQKRIIRHQPAATDILRLIELKIQDELRLPPIRPIRLLLSHNS 180
 QY 186 LLAIPFPIIPARVVALRIAGLGLGSDVDPSPRIANHLAWSDQLEKRVPPVIRGLRG 165
 DB 186 LLAIPFPIIPARVVALRIAGLGLGSDVDPSPRIANHLAWSDQLEKRVPPVIRGLRG 165
 DB 191 LLAIPGPIIPARVVALRIAGLGLGSDVDPSPRIANHLAWSDQLEKRVPPVIRGLRG 240
 QY 166 LTPIFLAGRTAGTPIPEPLACTAALQPIQVSNISLQATPVDSLTPIPLLLAAAPRPF 225
 DB 166 LTPIFLAGRTAGTPIPEPLACTAALQPIQVSNISLQATPVDSLTPIPLLLAAAPRPF 225
 DB 241 LTRIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIR 400
 QY 226 NQVPLSWPQVWPVPSHIVLASPEETPCHPKNAKPIILPIIYAFPGTATTTATVPT 285
 DB 226 NQVPLSWPQVWPVPSHIVLASPEETPCHPKNAKPIILPIIYAFPGTATTTATVPT 285
 DB 201 NQVPLSWPQVWPVPSHIVLASPEETPCHPKNAKPIILPIIYAFPGTATTTATVPT 460
 QY 286 TRVVVKEPRALSSSLAFTWLSQAPAFPAISPOSTAPPTVQVQVQVPSCLINGLIC 345
 DB 286 TRVVVKEPRALSSSLAFTWLSQAPAFPAISPOSTAPPTVQVQVQVPSCLINGLIC 345
 DB 362 LTRIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIRLQPIIR 420
 QY 346 HGTIRHRLACTCPPTGTGYCESQMGQTPSPPTVPPTPPTSLTIGIPVSPSTIRVGL 405
 DB 346 HGTIRHRLACTCPPTGTGYCESQMGQTPSPPTVPPTPPTSLTIGIPVSPSTIRVGL 405
 DB 421 HGTIRHRLACTCPPTGTGYCESQMGQTPSPPTVPPTPPTSLTIGIPVSPSTIRVGL 480
 QY 405 QPYLQSSSVLPSIPIIYPRISQVQVPIIIPASGLAIVYVQLKRAIVYQVQVMPHGP 465
 DB 405 QPYLQSSSVLPSIPIIYPRISQVQVPIIIPASGLAIVYVQLKRAIVYQVQVMPHGP 465
 DB 491 QPYLQSSSVLPSIPIIYPRISQVQVPIIIPASGLAIVYVQLKRAIVYQVQVMPHGP 540
 QY 466 GSVTQGLAIVYVQLKRAIVYQVQVMPHGP 525
 DB 466 GSVTQGLAIVYVQLKRAIVYQVQVMPHGP 525
 DB 541 QPYLQSSSVLPSIPIIYPRISQVQVPIIIPASGLAIVYVQLKRAIVYQVQVMPHGP 600
 QY 506 PPAAMAAAAPQGVVPMQAPPIIPVAVVPIIPKPAIVYQVQVMPHGP 585
 DB 506 PPAAMAAAAPQGVVPMQAPPIIPVAVVPIIPKPAIVYQVQVMPHGP 585
 DB 631 PPAAMAAAAPQGVVPMQAPPIIPVAVVPIIPKPAIVYQVQVMPHGP 690
 QY 586 PGLQSPPLIAKPYI 598
 DB 586 PGLQSPPLIAKPYI 598
 DB 661 PGLQSPPLIAKPYI 673

RESULT 6
 AAB87543
 ID AAB87543 standard; Protein: 673 AA.
 XX AAB87543.
 XX 15-MAY-2001 (first entry)
 XX Human PR01282.
 DE Human; PR0 protein; mapping.
 KW Homo sapiens.
 OS Homo sapiens.
 XX W0200116718-A2.
 XX

Db 419 hflldkhltpgadydclilalepaagpsdltatrlilgcakfstlpsapfcha:qahvlqgt 478
Qy 499 LPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAODKGOVGPGAGAGPLEGVK 553
Db 476 hv... avgtlraatlvftvally rgrg ...aguglflklshq 518

Search completed: September 17, 2002, 09:51:20
Job time: 1837 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 17, 2002, 09:26:23 Search time: 11.5 seconds
(without alignments)
100% 345 million cell updates/sec

Title: US-09-944-396-69
Perfect score: 3135
Sequence: 1 MCSRPVLLPILLILLALGK.....PLMGPPGRLQSLPILAKPYI 598

Scoring table: BLAST62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 2412594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:
1: US-09-063-950-2
2: US-09-063-950-5
3: US-09-063-950-6
4: US-09-063-950-7
5: US-09-063-950-8
6: US-09-063-950-9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3083.5	98.4	673	4	US-09-063-950-2
2	422	10.3	605	4	US-09-063-950-5
3	402	9.6	605	1	US-08-190-802A-49
4	302	9.6	605	4	US-08-477-346-49
5	302	9.6	605	4	US-08-473-089-49
6	298.5	9.5	649	4	US-09-188-930-305
7	281.5	9.0	603	1	US-08-190-802A-50
8	281.5	9.0	603	4	US-08-477-346-50
9	281.5	9.0	603	4	US-08-473-089-50
10	271.5	9.7	253	3	US-08-925-125-5
11	259	8.3	610	1	US-07-821-717B-6
12	259	8.3	610	1	US-08-119-262B-6
13	259	8.3	610	1	US-08-135-929A-11
14	259	8.3	610	1	US-08-344-265A-11
15	258	8.2	1523	4	US-09-182-024A-11
16	255.5	8.1	1480	4	US-09-191-647-7
17	255.5	8.1	1480	4	US-09-540-245A-7
18	255.5	8.1	1480	4	US-09-540-153-7
19	255.5	8.1	1480	4	US-09-182-024A-5
20	255.5	8.1	1480	4	PCT-US91-02055-2
21	247.5	7.9	1523	3	US-09-191-647-2
22	247.5	7.9	1523	3	US-09-540-245A-2
23	247.5	7.9	1523	4	US-09-540-153-2
24	244	7.8	708	4	US-09-131-648-2
25	240	7.7	560	3	US-08-592-509-2
26	240	7.7	560	3	US-08-592-509-2
27	240	7.7	560	4	US-09-063-950-4

29	240	7.7	560	5	PCT-US94-07644A-2	Sequence 2, Appl
29	236.5	7.5	232	5	PCT-US91-09055-4	Sequence 3, Appl
40	236.5	7.5	231	3	US-08-986-485-7	Sequence 7, Appl
31	225	7.2	735	4	US-09-191-647-9	Sequence 9, Appl
32	225	7.2	735	4	US-09-540-245A-9	Sequence 9, Appl
33	225	7.2	735	4	US-09-540-153-9	Sequence 9, Appl
34	222	7.1	196	5	PCT-US91-09055-5	Sequence 5, Appl
35	216.5	6.7	4352	3	US-08-628-136-7	Sequence 5, Appl
46	209	6.7	1041	3	US-08-986-485-5	Sequence 5, Appl
37	206.5	6.6	1101	3	US-08-986-485-2	Sequence 2, Appl
38	203.5	6.5	4303	3	US-08-480-751-2	Sequence 2, Appl
39	196.5	6.3	771	4	US-09-188-930-183	Sequence 183, App
40	193.5	6.2	224	5	PCT-US91-09055-4	Sequence 4, Appl
41	186.5	5.9	196	5	PCT-US91-09055-6	Sequence 6, Appl
42	184	5.9	320	1	US-07-614-084B-1	Sequence 1, Appl
43	179	5.7	368	1	US-08-592-239-3	Sequence 3, Appl
44	178	5.7	368	4	US-08-458-834-3	Sequence 3, Appl
45	175	5.6	368	6	5340934-2	Patent No. 5440934

ALIGNMENTS

RESULT 1
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND USES
; INVENTOR: Holtzman, Douglas A.
; PRIORITY CLAIM: PCT/US91-09055-4
; PUBLICATION NO.: 5340934-2
; SEQ ID NO: 2
; LENGTH: 673
; TYPE: Pct
; ORGANISM: Homo sapiens
US-09-063-950-2

Query Match	98.4%	Score 3083.5	DB 4	Length 673
Best Local Similarity	88.7%	Pct. No. 90-214		
Matches	592	Conservation	0	Mismatches 1
1	MCSRVPVLLPILLILLALGKVGCGCGSQGTPTVPTARQGTTPVPPVTVGLVYF	60		
DB	1	MCSRVPVLLPILLILLALGKVGCGCGSQGTPTVPTARQGTTPVPPVTVGLVYF	60	
QY	61	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	90	
DB	61	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	120	
QY	91	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	105	
DB	91	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	180	
QY	106	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	165	
DB	106	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	240	
QY	166	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	225	
DB	166	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	300	
QY	224	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	285	
DB	224	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	360	
QY	300	ENGHTMIDASSVAGLPGTGLLPLSONDIAS	345	
DB	300	ENGHTMIDASSVAGLPGTGLLPLSONDIAS		

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Db      361 TRVVVPEPTALSSAPTWISPTATAPASIPSTAPITVGPVQVQVCPSPSTCLNAGTC 420
QY      446 HLTTRHMLACGCEPTEGLYTESQMGCTRTSPVTVTHHPRSLTGLIEVSPSTSLRVL 405
Db      421 HLTTRHMLACGCEPTEGLYTESQMGCTRTSPVTVTHHPRSLTGLIEVSPSTSLRVL 480
QY      406 QRYLGSSVQLSPLELTVHNSGPKRLVILRLPASTAFYVTVGLRNATYSVCVMPILGP 465
Db      481 QRYLGSSVQLSPLELTVHNSGPKRLVILRLPASTAFYVTVGLRNATYSVCVMPILGP 540
QY      466 QVPPGCFEACGFPAHDDPAVNSHIAVTCAPESNPLLLIAPAAVLLAALAAVGAAYCVF 525
Db      541 GRVPEAFEACGFPAHDDPAVNSHIAVTCAPESNPLLLIAPAAVLLAALAAVGAAYCVF 600
QY      526 PPKAMAAAACGCEVQVPEACGPIETECVVPVPEFTTEVATEGCEPAIPGSEEFVTHMPTFG 585
Db      601 PPKAMAAAACGCEVQVPEACGPIETECVVPVPEFTTEVATEGCEPAIPGSEEFVTHMPTFG 660
QY      585 PQLQSPHAKPYI 563
Db      661 PQLQSPHAKPYI 673

RESULT 2
US-09-064-950-5
: Sequence 5, Application US/09063950C
: Patent No. 6225085
: GENERAL INFORMATION:
: APPLICANT: Hollmann, Douglas A.
: TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
: FILE REFERENCE: THEREFOR
: CURRENT APPLICATION NUMBER: US/09/063,950C
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 5
: LENGTH: 605
: TYPE: PRT
: ORGANISM: Papiio hamadryas
US-09-064-950-5

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Query Match      10 99: Score 422, db 4: Length 605
Best Local Similarity 36.2%; Pref. No. 2e-15;
Matches 100; Conservative 49; Mismatches 97; Indels 40; Gaps 11;

QY      7 LLLPILL--LALG-----PGVQG-----CPSGGQCQSQPQ-----TVFCTARQGIT 45
Db      8 LALALLLSWVALGPRSLGAPGTPGAEAGPACPAACVSYDDADRLSVFSSRNILTR 67
QY      46 VPPVPPPTVTHVYFENRTITMIDASSFACIPGLQITLIDSONQIASLRLPRLLL----- 98
Db      68 LPAAGTQALWISNNISIPVPAAPFNNISAFINLQSGQISLFP-PCALIGLFINLCH 126
QY      99 LDIHNSLLALEPGLDITANVIALKAGLS--LQQLRGLFSLRRLHLDVSDNQLER 155
Db      127 LHLERNGLSLAVTF--AYTALALIGLSNNLSRLKGLFEGGLNLDNLGNWSLAV 184
QY      156 VP-PVIRGLGLTRPLACNTHFACLEPEEDAGLAALGFTIIVSNLSLGLAPGSLGLPR 214
Db      185 LPDAARFGUGSLPFTVLVAGN-PLAYLQALFSGLAELPELDSLNRALRAKANVFAQLPR 243
QY      215 LRLAAARNPENCVPPLSMFG-----PWVPSFIVTIA 246
Db      244 LQKLYLDRNLIAAVAGAFGLKALRWLDLSNRVA 279

RESULT 3
US-08-190-802A-49
: Sequence 49, Application US/09190802A
: Patent No. 5619004
: GENERAL INFORMATION:
: APPLICANT: Mochly-Kosen, Darla

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Query Match      9.6%; Score 402; DB 1: Length 605;
Best Local Similarity 40.9%; Pref. No. 4e-14;
Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

QY      7 LLLPILL--LALG-----PGVQG-----CPSGGQCQSQPQ-----TVFCTARQGIT 45
Db      8 LALALLLSWVALGPRSLGAPGTPGAEAGPACPAACVSYDDADRLSVFSSRNILTR 67
QY      46 VPPVPPPTVTHVYFENRTITMIDASSFACIPGLQITLIDSONQIASLRLPRLLL----- 98
Db      68 LPAAGTQALWISNNISIPVPAAPFNNISAFINLQSGQISLFP-PCALIGLFINLCH 126
QY      99 LDIHNSLLALEPGLDITANVIALKAGLS--LQQLRGLFSLRRLHLDVSDNQLER 155
Db      127 LHLERNGLSLAVTF--AYTALALIGLSNNLSRLKGLFEGGLNLDNLGNWSLAV 184
QY      156 VP-PVIRGLGLTRPLACNTHFACLEPEEDAGLAALGFTIIVSNLSLGLAPGSLGLPR 214
Db      185 LPDAARFGUGSLPFTVLVAGN-PLAYLQALFSGLAELPELDSLNRALRAKANVFAQLPR 243
QY      215 LRLAAARNPENCVPPLSMFG-----PWVPSFIVTIA 246
Db      244 LQKLYLDRNLIAAVAGAFGLKALRWLDLSNRVA 279

RESULT 4
US-08-477-346-49
: Sequence 49, Application US/08477346
: Patent No. 6262023
: GENERAL INFORMATION:
: APPLICANT: Mochly-Kosen, Darla

```

```

1  APPLICANT: Ron, Dorit
2  TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
3  TITLE OF INVENTION: Theof
4  NUMBER OF SEQUENCES: 255
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Morrison & Foerster
7  STREET: 2000 Pennsylvania Avenue, NW
8  CITY: Washington
9  STATE: DC
10 COUNTRY: USA
11 ZIP: 20006-1812
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US 09/477,346
19 FILING DATE: 07-JUN-1995
20 CLASSIFICATION: 514
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 09/487,072
23 FILING DATE: 07-JUN-1995
24 ATTORNEY/AGENT INFORMATION:
25 NAME: MURASHIGE, KATE H.
26 REGISTRATION NUMBER: 24,959
27 REFERENCE/INVENT NUMBER: 255-396-69
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (202) 887-1500
30 TELEFAX: (202) 887-0763
31 INFORMATION FOR SEQ ID NO: 49:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 605 amino acids
34 TYPE: amino acid
35 TOPOLOGY: unknown
36 MOLECULE TYPE: protein
37 HYPOTHEICAL: NO
38 ANTI-SENSE: NO
39 ORIGINAL SOURCE:
40 INDIVIDUAL ISOLATE: Insulin like growth factor binding
41 INDIVIDUAL ISOLATE: protein complex, Fig. 32
42 US-08-477-446-49

```

```

Query Match          9 68; Score 302; DB 4; Length 605;
Best Local Similarity 25.58; Prod. No. 5.4e-14;
Matches 98; Conservative 40; Mismatches 58; Indels 40; Gaps 11;

7  LLLPLLLL--LALG-----PGVQG-----GPSGCGCSQPQ-----IVFCTARQGIT 45
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8  LALALLLSWVAIGPRSTEGADPTGAEAGPAPACACVSYDDDADELSEVCSNNLTK 67

46  VPRVPPPTVGLVFEENITMDASSFAGLPGGLLDLSONOIASLRLLPRLLL----- 98
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68  LPDVGPGTQALWLDGNNISVVVAAAFQNISSLCFTIRLQGGQGLSE--PQALLGLNLUCH 126

99  LILSHNSLLALEPGILDTANVEALPLAAGLG---LQNI DEGI FSPRLNHLVSDNQLER 155
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127  LHLERNQLPSALCTF--AHTPALASLGLSNNPISRLDGLFEGISGLMDNLGNWSLAV 184

156  VP-PVIRGLRGLRLRACNTRTAGI RPDIAAGI AALQELDVSNLSIQAIPGLLSGLFPR 214
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185  LPDAAFPGIGSRLRLVAGN--RLAYIQALFSLGLAEIRLELDSKNALRAIKANVVFQVLR 243

215  LRLAAARNPNCVPLSWFG---PWRRESHVTLA 246
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244  LKLYLLENLLAAVAPGAFGLKALPWLIDLSHNEVA 279

```

```

RESULT 5
US-08-477-446-49
; Sequence 49, Application US/08473089
; Patent No. 6342368

```

```

1  GENERAL INFORMATION:
2  APPLICANT: Mechly-Rosen, Daria
3  APPLICANT: Ron, Dorit
4  TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
5  TITLE OF INVENTION: Theof
6  NUMBER OF SEQUENCES: 265
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Morrison & Foerster
9  STREET: 2000 Pennsylvania Avenue, NW
10 CITY: Washington
11 STATE: DC
12 COUNTRY: USA
13 ZIP: 20006-1812
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: 09/487,473,089
21 FILING DATE: 07-JUN-1995
22 CLASSIFICATION: 435
23 ATTORNEY/AGENT INFORMATION:
24 NAME: MURASHIGE, KATE H.
25 REGISTRATION NUMBER: 29,959
26 REFERENCE/INVENT NUMBER: 255-396-69
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (202) 887-1500
29 TELEFAX: (202) 887-0763
30 INFORMATION FOR SEQ ID NO: 49:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 605 amino acids
33 TYPE: amino acid
34 TOPOLOGY: unknown
35 MOLECULE TYPE: protein
36 HYPOTHEICAL: NO
37 ANTI-SENSE: NO
38 ORIGINAL SOURCE:
39 INDIVIDUAL ISOLATE: Insulin like growth factor binding
40 INDIVIDUAL ISOLATE: protein complex, Fig. 32
41 US-08-473-089-49

```

```

Query Match          9 68; Score 302; DB 4; Length 605;
Best Local Similarity 25.58; Prod. No. 5.4e-14;
Matches 98; Conservative 40; Mismatches 58; Indels 40; Gaps 11;

7  LLLPLLLL--LALG-----PGVQG-----GPSGCGCSQPQ-----IVFCTARQGIT 45
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8  LALALLLSWVAIGPRSTEGADPTGAEAGPAPACACVSYDDDADELSEVCSNNLTK 67

46  VPRVPPPTVGLVFEENITMDASSFAGLPGGLLDLSONOIASLRLLPRLLL----- 98
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68  LPDVGPGTQALWLDGNNISVVVAAAFQNISSLCFTIRLQGGQGLSE--PQALLGLNLUCH 126

99  LILSHNSLLALEPGILDTANVEALPLAAGLG---LQNI DEGI FSPRLNHLVSDNQLER 155
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127  LHLERNQLPSALCTF--AHTPALASLGLSNNPISRLDGLFEGISGLMDNLGNWSLAV 184

156  VP-PVIRGLRGLRLRACNTRTAGI RPDIAAGI AALQELDVSNLSIQAIPGLLSGLFPR 214
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185  LPDAAFPGIGSRLRLVAGN--RLAYIQALFSLGLAEIRLELDSKNALRAIKANVVFQVLR 243

215  LRLAAARNPNCVPLSWFG---PWRRESHVTLA 246
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244  LKLYLLENLLAAVAPGAFGLKALPWLIDLSHNEVA 279

```

```

RESULT 6
US-09-188-930-305
; Sequence 305, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:

```

1 APPLICANT: Watson, James D.
 2 APPLICANT: Strachan, Lorna
 3 APPLICANT: Sleeman, Matthew
 4 APPLICANT: Onrust, Rene
 5 APPLICANT: Murlison, James Greg
 6 TITLE OF INVENTION: Compositions Isolated From Skin Cells
 7 TITLE OF INVENTION: and Methods For Their Use
 8 FILE REFERENCE: 11000.1011c1
 9 CURRENT FILING DATE: 1998-11-09
 10 NUMBER OF SEQ ID NOS: 348
 11 SOFTWARE: FASTSEQ for Windows Version 3.0
 12 SEQ ID NO 405
 13 LENGTH: 649
 14 TYPE: PRT
 15 ORGANISM: Mouse
 16 US-09-188-940-305

Query Match 9.5%; Score 298.5; DB 4; Length 649;
 Best local Similarity 22.8%; Pred. No. 1,10-13;
 Matches 141; Conservative 80; Mismatches 220; Indels 177; Gaps 23,
 22 GQPSGQCSQGPVPTVPTARQGTTHVVPDVGGLY- 58
 26 KQSPVPS-DAGFVYCHQSTSTVATVATVYQDR-IRHVGTHESLKLKVE 87
 59 -----VFENGITLMDASSFAGIPGQIIDLSONGLASLRLPP 95
 88 LVHNSLGIPTNLKFFVNFHGFNNITTTTSLSPFPLEELHNSVSAVTEE 147
 96 -----LILLDSHNSLALPGIIDLANVEALRLAG- 126
 148 GAFRUSNYLRLFLSNHLSITWQIPRT--TEFLPDNRTISTSSPLGLTSLKPLV 205
 127 -- --LCLQQLDELSRLNHLIVSNQLEPVPVPIPELPGITPLPLACNTRIAGLR 181
 206 LDGNLLNHHGIGUKVFNINTELSLVNSUTAAAPVNLPG-TSLKRLYLQDN-HINRVP 263
 182 PDIAGIAALQFIVNSISQALPDLGLDELELLAAAPNPNVGLPSWFGHWVES 241
 264 PRAFSLRLGLFLMSNNLSLFGTHHIDNITCIILERNWYGGKMKWVRLQSL 323
 242 HVTLASFFTHQHPKNAPIIIFIDVADPGCAPATTATVPTPPVVPPEPTALSSSLA 301
 424 PVKV-NVRHIM-CAPEKVVGMALKLSAELECKDSGIVSTIQT-----TAT----- 370
 402 PTWISPTAPATEAPSPPTAPTVG--PVP---QPQDPPSTCLNGGICHLGTRHHLACL 356
 471 -----PNTAYAGQGMVADPVTKQPKNPKLRD----- 399
 457 QPEFTGLCVESONGGTREPTPTVTPFRFSLILGIEFVSPISLRVSLGRYLQSSVQL 416
 400 -----ORTGSPS-----PKTILITVSVTPVTHHSRLALPMTALRL 438
 417 RSLRLITRNLSGP-DRKLVTLKPLASLARYVTQLRPNATYSVCMPLGPKVPEGE-- 473
 439 SWLKIGHSFAFGSITETIVT----GERSEYLVTALEPESPRVCMVPMETSNLYIFDETP 494
 474 ACCEAHIPPAVESHNAVPT--GAFS-----GNLPL--LIAPALAAVLAAALAAVCAAY 522
 495 VCLETQAPLRMYN--PTTINPEQKEPKYKNPNPLAATIGGAVALVSIALLALV-CWY 551
 523 CVRGRAMAA-AAQDKGQ 539
 552 VIKNGSLFSKNCAYSKGR 569

RESULT 7
 US-08 190 802A-50
 : Sequence 50, Application US/09160902A
 : Patent No. 5519003
 : GENERAL INFORMATION:

1 APPLICANT: Mochly-Rosen, Daria
 2 APPLICANT: Ron, Dorit
 3 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 4 TITLE OF INVENTION: Thereof
 5 NUMBER OF SEQUENCES: 265
 6 CORRESPONDENCE ADDRESS:
 7 ADDRESSEE: Dehlinger & Associates
 8 STREET: P.O. Box 60850
 9 CITY: Palo Alto
 10 STATE: CA
 11 COUNTRY: USA
 12 ZIP: 94306-0850
 13 COMPUTER READABLE FORM:
 14 MEDIUM TYPE: Floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC-DOS/MS-DOS
 17 SOFTWARE: PatentIn Release #1.0, Version #1.25
 18 CURRENT APPLICATION DATA:
 19 APPLICATION NUMBER: US/08/190,802A
 20 FILING DATE: 01-FEB-1994
 21 CLASSIFICATION: 530
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: Fabian, Gary R.
 24 REGISTRATION NUMBER: 33,875
 25 REFERENCE/DOCKET NUMBER: 8600-0139
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: (415) 324-0880
 28 TELEFAX: (415) 324-0960
 29 INFORMATION FOR SEQ ID NO: 50:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 603 amino acids
 32 TYPE: amino acid
 33 TOPOLOGY: unknown
 34 MOLECULE TYPE: protein
 35 HYPOTHETICAL: NO
 36 ANTI-SENSE: NO
 37 ORIGINAL SOURCE:
 38 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 39 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 40 US-08-190 802A-50

Query Match 9.0%; Score 281.5; DB 1; Length 603;
 Best local Similarity 32.4%; Pred. No. 1,60-12;
 Matches 92; Conservative 49; Mismatches 106; Indels 47; Gaps 11;
 QY 6 PLILPLILL-LALGP-GVGG-----GSGGTCQSQPO-----TVETARQETT 45
 DB 8 PALVILLATWVALPGCHLOGTDFGASIAEGQCPVACTSHDDYDLSVFSKKNLTH 67
 QY 46 VPRDVPDPTVGLVVPFNGITMLDASSFAGIPGQIIDLSONGLASLRLPP-----LPRILL 99
 DB 6R LPDIPVSPRALWIPGNNISIPSAAPNLSIPFNIQSWIPSPQALGQNYVI 127
 QY 100 DLSHNSLALPGIIL-DTANVEALKIAGLIGLQGLHESLRLHLDLVCTHOLRVP-- 157
 DB 128 HLEPNPLRLNVLWGLTHETPTSLASLSLSSNLGLPFEELFGLSHLDLNGWNSLVLPD 187
 QY 15R PVTIRCPCTPTPLPNTPTAGIPPTIAGIAATGFTIVSNISLQALNGLSLFLRKL 217
 DB 188 TVPQGLNHLVLAQGN-KLITYLQALPGGLGELBELDLSNALSRYKANNVHILPQIK 246
 QY 218 LAAARNPNCVPLSWFG----PWVRESVHTLAS-PEETRCHEFP 256
 DB 247 LYLDRLNLTAVAGAFGLGMKALRWLDLSHNRVAGLMEDT---FP 287

RESULT 8
 US-08-477-346-50
 : Sequence 50, Application US/08477346
 : Patent No. 626203
 : GENERAL INFORMATION:
 : APPLICANT: Mochly-Rosen, Daria

Db 4 CEVSKVASHLEFVNCKENLIALPDLPKDTTILHSENLLYTSLSATLMPYTRITQNLND 63
QY 71 SF-----AGLPRIQLIDISQNTASL-----PIPPILLIDLSHNSLLALEPGILNTA 117
Db 64 RCFETKLVQVGLFIEVDRITGSHKQSGLELLQGLIPALIVLAVSNPFTLSIPIG----- 118
QY 118 NVEALRLAGLGLGLDEGLDFSRIPNHHGVSNKLEKPPV-VIPGIPKLEPIKLANINP 176
Db 119 ---ALR-GLG-----ELQELYKVNELKTIPPGLITPPKPKRISIA-NNN 159
QY 177 IAQLRPEDLAGLAALQFQVSNISIALPQMLSG--LFFPLFTIAAAPNFRVQVLSWP 234
Db 160 LTFPVGILLNGLENDLILLQNSLYTIKPGFPGSHLPFAFLHG---NFWLNCDELIF 216
QY 235 GPWVRES---HVTLASPEETPC-----HPPPNAGRLLE--LDYA 270
Db 217 SFNKGQANFVWVWQGVVAKAMISWASVQDREKRFVYKFGKGLDQDFQITLY 276
QY 271 DEFCATATTATVTPTRVVFEP-----TALSSELAPFWLSPFAFIE-- 313
Db 277 DYVEEDTEGDKVRAFTVVKFTKAKHTFWSGLFYSWSIASLDSQMSLSHPTQESTKE2 346
QY 314 -----APPPSTAPPTVGPV--PQGGQCPPESTCINGSGFCHGIR 350
Db 337 TTFPPWPTNFILHMSITFSKTPKSTETPTSPFTTSEPVVEFAPNMTLEPT----- 390
QY 351 HHIACTQPEGFGLGYSQWQDRIKPSPTVTPPPPSLTLGIFP---VSPSLRVCLQP 407
Db 391 ---SPTPE-----PISEPAPSTPEPTPIPTIATSPILYSATLSLTPKST 435
QY 408 YLOGSS-VOLPSRLTYRNLSPDKPIVTP--LPASLAETVITLPPRNATYSVQVMP 463
Db 436 FLTTKPVSLSEKKTIFELQGFKLKGVLGHLLESSKRL-FLHED---PQULLL 489
QY 464 Q-----PGV-PPCPACQCAHTPPPAVHSHADVTQAPRGNIP 500
Db 466 GFVYVIGFMI FASWVILLISWVHVKEGALINSQGAALTATATTHLELQGFQAVTP 549
QY 501 ---LLI---APALAAVLLAALAAVGAAYGVRRGRAMAAADKQ 539
Db 550 KAWILFPGSIPTEPSSIFVWPINPVGPIVAGPPHVSLSQGRQ 595

RESULT 12

US-08-119-262B-6

Sequence 6, Application US/08119262B

Patent No. 5492809

GENERAL INFORMATION:

APPLICANT: Miller, Jonathan I.

APPLICANT: Cunningham, David

APPLICANT: Lyle, Vicki A.

APPLICANT: Finch, Clara N.

TITLE OF INVENTION: MUTATIONS AFFECTING PLATELET

TITLE OF INVENTION: GLYCOPROTEIN Ib ALPHA LESS REACTIVE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Nixon, Hargrave, Devaux & Bayle

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1 0, Version #1 30

CURRENT APPLICATION DATA:

APPLICATION NUMBERS: US-08/119-262B

FILING DATE: 09-SEP-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 01/821,717

ATTORNEY/AGENT INFORMATION:
NAME: Timlin, Susan J.
REGISTRATION NUMBER: 34,103
PENDING/PACKET NUMBER: 40684/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Lopez, Jose A.
AUTHORS: Chung, Dominic W.
AUTHORS: Fujikawa, Kazuo
AUTHORS: Hagen, Frederick S.
AUTHORS: Papayannopoulos, Thalia
AUTHORS: Koth, Gerald J.
TITLE: Cloning of the alpha chain of human platelet
glycoprotein Ib: A transmembrane protein
TITLE: Leucine rich alpha 2 glycoprotein
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 84
PAGES: 5615-5619
DATE: AUG-1987
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610
PUBLICATION INFORMATION:
AUTHORS: Zimmerman, Theodore S.
AUTHORS: Kugger, Zaverio M.
AUTHORS: Houghten, Richard A.
AUTHORS: Vincete, Vincete
AUTHORS: Mohri, Hiroshi
TITLE: Proteolytic fragments and synthetic peptides
TITLE: that block the binding of von Willebrand
factor to
membrane glycoprotein Ib
DOCUMENT NUMBER: EP 0 317 278 A2
FILING DATE: 16-NOV-1988
PUBLICATION DATE: 24-MAY-1989
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293
US-08-119-262B-6

Query Match 8.38; Score 259; DB 1; Length 610;

Best Local Similarity 24.18; Pred. No. 6,7e-11;

Matches 156; Conservative 72; Mismatches 249; Indels 188; Gaps 28;

QY 28 CQCSQPT--VECTARQCTVIRGVVPTVGLVYVEN-----GITMLDAS 70
Db 4 CEVSKVASHLEFVNCKENLIALPDLPKDTTILHSENLLYTSLSATLMPYTRITQNLND 63
QY 71 SF-----AGLPRIQLIDISQNTASL-----PIPPILLIDLSHNSLLALEPGILNTA 117
Db 64 RCFETKLVQVGLFIEVDRITGSHKQSGLELLQGLIPALIVLAVSNPFTLSIPIG----- 118
QY 118 NVEALRLAGLGLGLDEGLDFSRIPNHHGVSNKLEKPPV-VIPGIPKLEPIKLANINP 176
Db 119 ---ALR-GLG-----ELQELYKVNELKTIPPGLITPPKPKRISIA-NNN 159
QY 177 IAQLRPEDLAGLAALQFQVSNISIALPQMLSG--LFFPLFTIAAAPNFRVQVLSWP 234
Db 160 LTFPVGILLNGLENDLILLQNSLYTIKPGFPGSHLPFAFLHG---NFWLNCDELIF 216
QY 235 GPWVRES---HVTLASPEETPC-----HPPPNAGRLLE--LDYA 270
Db 217 SFNKGQANFVWVWQGVVAKAMISWASVQDREKRFVYKFGKGLDQDFQITLY 276
QY 271 DEFCATATTATVTPTRVVFEP-----TALSSELAPFWLSPFAFIE-- 313
Db 277 DYVEEDTEGDKVRAFTVVKFTKAKHTFWSGLFYSWSIASLDSQMSLSHPTQESTKE2 346
QY 314 -----APPPSTAPPTVGPV--PQGGQCPPESTCINGSGFCHGIR 350
Db 337 TTFPPWPTNFILHMSITFSKTPKSTETPTSPFTTSEPVVEFAPNMTLEPT----- 390
QY 351 HHIACTQPEGFGLGYSQWQDRIKPSPTVTPPPPSLTLGIFP---VSPSLRVCLQP 407
Db 391 ---SPTPE-----PISEPAPSTPEPTPIPTIATSPILYSATLSLTPKST 435
QY 408 YLOGSS-VOLPSRLTYRNLSPDKPIVTP--LPASLAETVITLPPRNATYSVQVMP 463
Db 436 FLTTKPVSLSEKKTIFELQGFKLKGVLGHLLESSKRL-FLHED---PQULLL 489
QY 464 Q-----PGV-PPCPACQCAHTPPPAVHSHADVTQAPRGNIP 500
Db 466 GFVYVIGFMI FASWVILLISWVHVKEGALINSQGAALTATATTHLELQGFQAVTP 549
QY 501 ---LLI---APALAAVLLAALAAVGAAYGVRRGRAMAAADKQ 539
Db 550 KAWILFPGSIPTEPSSIFVWPINPVGPIVAGPPHVSLSQGRQ 595

```

QY 314 ----- APSPESTAPPTVGPV---PQDQCPPTCINGCTCHLCTR 360
Db 337 TTPPPHWTFNLHMESITFSKSTSTPTSTISGPVPEPAPNMITUEPTP----- 390
QY 351 HMLACLPFGTGLACESQWCGTGRPSPTVPTRPPESTITIGTFP---VSPSTSLFVRIQR 407
Db 391 ---SPTTPE-----PTSEPAESPITPTPTPTIATSPTHIVSATSLITPKST 435
QY 408 YLGSS--VQIHSRHTYNNISGPCKPLVTLR--LPASLAFTVTVQLFPNATYSVCMPL 463
Db 436 EHTTIVWVLESTRETDETCQPKELPMVQCHIFSEFND PFELHES---PFTCLIFL 489
QY 464 G-----PCRV-PESEFAN*GEAHTPPAVHSNHAFVTAKEGNLP 500
Db 490 GFYVIGLEFWLIFASVLLILSWVSHVKKPQALDSQGAALITATQTHIELQRPQVTVP 549
QY 501 ---LLI---APALAAVILAAIAAAGAAAYGVRRGKAMAAAQIKSQ 539
550 PAMILFIPGSIPTPSSSIFVWPPNCPVCPVAGPPPSALSQCPQ 595

RESULT 13
US-08-135-929A-11
: Sequence 11, Application US/08135929A
: Patent No. 5593959
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan L.
: APPLICANT: Cunningham, David
: APPLICANT: Lyle, Vicki A.
: APPLICANT: Finch, Clara N.
: APPLICANT: Pincus, Matthew R.
: TITLE OF INVENTION: Mutations in the Gene Encoding the Alpha
: TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle
: STREET: Clinton Square, P.O. Box 1051
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/135,929A
: FILING DATE: 14-OCT-1993
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Timian, Susan J.
: REGISTRATION NUMBER: 34,103
: REFERENCE/POCKET NUMBER: 26984/23
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (716) 263-1636
: TELEFAX: (716) 263-1600
: TELEX: 978450
: INFORMATION FOR SEQ ID NO. 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 610 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-135-929A-11

```

```

Query Match: 8 34: score 259; DB 1: Length 610;
Best Local Similarity 24.14; Pred. No. 6.7e-11;
Matches 146; Conservative 72; Mismatches 230; Inlets 188; Gaps 28.
QY 28 CQCSQPT---VCTARQTTVPDVPDPTVGLVFFEN-----GITMLDAS 70

```

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Db 4 CEVSKVASHLEWVCEKFNILIALPPLPKDTTILHISENLATYSLATIMYTRITQLNLD 63
QY 71 SF-----AGLPQLQLLDLSQNGIASL-----KLPLQLLLDLSHSLALAGPGLIITA 117
Db 64 ECELIKEDVNDGTPLVLTITPLSHNGSQSEPLTIGOTLEALTVDVSNFRSLTSLPAG----- 118
QY 118 NVEALPLACLGLOQLDEGLFSPIPNLHDLVSNQCEPVPD-VIWCPLGLTLPGLACNTR 176
Db 119 ---ALR---GLG-----ELQELYKVNELKTLPLGGLLITPKLKRISIA-NNN 159
QY 177 TAC EFCETAYLAIAIQLFVHISICALPTTFC IPTTSFELAAAFHTFHWVTSWMP 234
Db 160 LLELPLVGLINGLENLTLLIQFNSLYTTPKGFPSHLLPFAFIHQ---NWLQNFILYF 216
QY 235 GHWVES-----HYTLASPTTFC-----HEPKNACPLILP--LDYA 270
Db 217 PFWLQUNAFNVYVMKQGVIVAKAMISNVA5VQUNSLQKFPYKYCKSPITGPRSTIY 276
QY 271 DFGCPATTTATVPTTPVPVREP-----TALSSSLAPTLSPITAPATE-- 313
Db 277 DYPEDTSGUKVPATKIVVFPPTZAHITLFWELFYSNSTASIDSMFSSITPTQPSSTFQ 336
QY 314 -----APSPSTAPPTVGPV---PQDQCPPTCINGCTCHLCTR 350
Db 337 TTPPPHWTFNLHMESITFSKSTSTPTSTISGPVPEPAPNMITUEPTP----- 390
QY 351 HMLACLPFGTGLACESQWCGTGRPSPTVPTRPPESTITIGTFP---VSPSTSLFVRIQR 407
Db 391 ---SPTTPE-----PTSEPAESPITPTPTPTIATSPTHIVSATSLITPKST 445
QY 408 YLGSS--VQIHSRHTYNNISGPCKPLVTLR--LPASLAFTVTVQLFPNATYSVCMPL 463
Db 436 EHTTIVWVLESTRETDETCQPKELPMVQCHIFSEFND PFELHES---PFTCLIFL 489
QY 464 G-----PCRV-PESEFAN*GEAHTPPAVHSNHAFVTAKEGNLP 500
Db 490 GFYVIGLEFWLIFASVLLILSWVSHVKKPQALDSQGAALITATQTHIELQRPQVTVP 549
QY 501 ---LLI---APALAAVILAAIAAAGAAAYGVRRGKAMAAAQIKSQ 539
Db 550 PAMILFIPGSIPTPSSSIFVWPPNCPVCPVAGPPPSALSQCPQ 595

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RESULT 14
US-08-234-265A-11
: Sequence 11, Application US/08234265A
: Patent No. 5624817
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan L.
: APPLICANT: Cunningham, David
: APPLICANT: Lyle, Vicki A.
: APPLICANT: Finch, Clara N.
: APPLICANT: Pincus, Matthew R.
: TITLE OF INVENTION: Mutations in the Gene Encoding the
: TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle
: STREET: Clinton Square, P.O. Box 1051
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1 25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/234,265A
: FILING DATE: 28-APR-1994
: CLASSIFICATION: 536

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: TITLE OF INVENTION: Homo Slit Polypeptide and Polymers thereof
: TITLE OF INVENTION: Same
: FILE REFERENCE: 640190-271
: SUB-OR: APPLICATION NUMBER: US 09/182,624A
: CURRENT FILING DATE: 1998-10-29
: PRIOR APPLICATION NUMBER: 60/063,946
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/096,420
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1523
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-182-024A-2

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A:Title: Isolation and characterization of human blood platelet mRNA and construction of a GPIb coding cDNA insert.
 A:Reference number: A60435; MIM:90920160
 A:Accession number: A60435
 A:Molecule type: mRNA
 A:Residues: 1-605 <LE0>
 A:Cross-references: GR:068626; RID:j184807; PID:AAA36347.1; PID:q184808
 A:Experimental source: liver
 A:Note: sequence extracted from NCHI backbone (NCHI:110171)
 C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
 F:94-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE1>
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 F:124-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE2>
 F:124-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE2>
 F:171-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE3>
 F:171-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE3>
 F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE4>
 F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE4>
 F:195-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE5>
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 F:216-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE6>
 F:216-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE6>
 F:244-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE7>
 F:244-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE7>
 F:267-296/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE8>
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 F:291-317/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE9>
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 Best local Similarity 35.5%; Pred. No. 2,7e-10;
 Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

QY 7 LLLPLLLL-LALG-----RCVQ-----CPSGQCSQPQ-----TVCETARQGT 45
 Db 8 LALALLLLSWALGRSLGADHGTCEARGPACACVCSYDIADELSEVCSRSK 67

QY 46 VPRVPPPTVTVYVFNEITMDIASSFALPLGLQLLDLSNDIASIPLPRILL----- 98
 Db 68 LPRVPGTGMALDGNSSVPPAAFNLSSTGFIHQDQNGSLF-PDALIGFENLCH 126

QY 99 LDISSNLLALPGIITDANVFALRLAGL-----IQQDRLVLSPLPNIHLDVSNQLEP 155
 Db 127 LHLERNLGRSLATPE-AHTPALASLGSNNRSLSPLEMLLEGLSGSELNLSWNSLAV 184

QY 156 VVPTVPLQLVTPFLACHTFPAQLFPIELALALALGLQVSNHSLSLALPGLSLLETF 214
 Db 185 LPIAALPGLGSGSPHVIARN-PAATGPALEFSLAFEPFPI SPNALPAIFANVPLVPLP 242

QY 215 FFLAAAFNIPVPTVSWPS FVWRFSHVTLA 246
 Db 244 LQVIVIDPNI LAAVAPAPLGLFALPRLDLSHPVA 276

RESULT 3
 NR001A
 platelet glycoprotein Ib alpha chain precursor - human
 N:Alternate names: membrane glycoprotein Ib alpha chain
 N:Contatus: glyvocalcin
 C:Species: Homo sapiens (man)
 C:Date: 28-Dec-1987 #sequence_revision 28 Dec 1987 #rev_change 22 Jun 1999
 A:Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102
 R:Lepeck J.A.; Choud B.W.; Fujikawa K.; Hagen F.S.; Papayannopoulos, T.; Poth, G. I
 Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
 A:Title: Cloning of the alpha chain of human platelet glycoprotein Ib: a transmembrane
 A:Reference number: A94174; MIM:87289655
 A:Accession: A94174
 A:Molecule type: mRNA
 A:Residues: 1-626 <LE0>
 A:Cross-references: GR:102940; NID:q183499; PID:AAA52595.1; PID:q306793
 R:Wick, A. N.; Walz, A.; Gerlach-Huber, S. N.; Wengler, F. H.; Vothhagen, K.
 Thromb. Haemost. 61, 448-453, 1989

A:Title: Isolation and characterization of human blood platelet mRNA and construction of a GPIb coding cDNA insert.
 A:Reference number: A60435; MIM:90920160
 A:Accession number: A60435
 A:Molecule type: mRNA
 A:Residues: 257-467 <WIC>
 R:Titani, K.; Takio, K.; Honda, M.; Kuwajiri, Z. M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
 A:Title: Amino acid sequence of the von Willebrand factor binding domain of platelet
 A:Reference number: A94173; MIM:87289654
 A:Accession: A94173
 A:Molecule type: protein
 A:Residues: 17-315 <TIF>
 R:Hess, G.; Schaller, C.; Fritsch, E. F.; Vercells, G. F. J.
 Eur. J. Biochem. 199, 389-393, 1991
 A:Title: Identification of the His-tagged bands in human platelet glyvocalcin.
 A:Reference number: S16945; MIM:91301149
 A:Accession: S16945
 A:Molecule type: protein
 A:Residues: 254-276, 276-277, 281-282, 282-283
 R:Lepeck J.A.; Ledwith, E.B.; McCarthy, B.J.
 J. Biol. Chem. 267, 15055-15061, 1992
 A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
 A:Accession number: I55355; MIM:92250564
 A:Status: preliminary
 A:Molecule type: DNA
 A:Cross-references: GR:S34435; NID:3249376; PID:AA0221211; PID:q4249177
 A:Note: variant D
 C:Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participa
 C:Comment: Platelet activation apparently involves disruption of the macromolecular c
 C:Comment: Binding sites for von Willebrand factor and thrombin (the latter site with
 C:Comment: Glyvocalcin, which is approximately coextensive with the extracellular pa
 C:Genetics:
 A:Gene: GDB:GPIB; GPIB
 A:Cross-references: GDB:118809; MIM:231200
 A:Map position: 17pter-17p12
 C:Complex: heterodimer with platelet glycoprotein Ib beta chain (NR001B)
 C:Superfamily: platelet glycoprotein Ib alpha chain; leucine rich alpha 2 glycoprotein
 C:Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem r
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MT>
 F:48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE1>
 F:72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE2>
 F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE3>
 F:117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE4>
 F:141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE5>
 F:165-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE6>
 F:189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE7>
 F:229-430/Domain: proline/threonine-rich 9 residue repeats
 F:502-540/Domain: transmembrane #status predicted <TM>
 F:541-626/Domain: intracellular #status predicted <INT>
 F:57-176/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 9.0%; Score 282; PB 1; Length 626;
 Best local Similarity 24.0%; Pred. No. 4.1e-09;
 Matches 169; Conservative 72; Mismatches 244; Indels 199; Gaps 26;

QY 9 LPLTLLTALPGVPTVSWPS FVWRFSHVTLA 246
 Db 1 MPLLLLLLLLPSLPHPPTVSWPSKVASHLVNTGENTALLPDLKPLIHLSENLLY 60

QY 63 -----GTMIDASSF-----AGLPGLQLLDLSNDIASIPLPRILL 98
 Db 61 TFSIATMPYPTVQLNLPVCFILQVQVCTIVLSTIQLSHNQTSQSLIQLTFLATV 120

QY 59 LQSHSLALFNHITANVPALELAGLGLQVSNHSLSLALPGLSLLETF 157
 Db 59 LQSHSLALFNHITANVPALELAGLGLQVSNHSLSLALPGLSLLETF 157

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121 LAAVNRSLTSLVAAERGHGTHLVKRPHTVTPFGLTTTPKPKLGAIRNTPLPDR
Q1 159 FVTHVREHTEFAGNTHIAGLEPHTIAQAAQGLWNLGALALALSSITFP114
Db 181 AGLLNGLNLTLLQEN-----SLVTPKQFTCSHLHFF215
Q2 215 IRLAAARPRVCTLSWTFWVER-----HVTASPTTSC-----253
Db 216 ARIHQ---NPWLCHETLITFPWQGNAPRVVWVGVVFAKPSHWAVVTHRSKRPV272
Q3 254 -RTHVNAERLLIE-LVAHFOCATTTATVTHVWER-----IA295
Db 273 KVPKGGTLLCHETHTAVVAFPTTTPGAVETAVVFLPAAFLWGLVSWSTA432
Q4 296 LSSSLAPLWLSPTAPE-----APSPSTAPITVGPV---PD340
Db 333 SLDSQMSLSEPTSEKTPETPPPPWNTPLHWPSTKSTKSTPTPTPTSPV362
Q5 331 FQDQSTFCLNETHETREHIALCFRPTETVYKESMGQTPPTSPVTPPPSPST390
Db 393 PPAPVNMHTTTPD-----SPITPR-----PTSPAPSTPTPTPTPT431
Q6 391 LGHPD---VSPSTLPGVLOPYLGSS-VQVPSIPITVPLNSGHPKVLVLP--LEASLA443
Db 432 IATSTILVASTLSITKSTLTITFVSLSESTKTKTLPGLVGLQSHLESSR491
Q7 444 EYVITQLPNAIYSWVMPLE-----PPFVPEGLAAGEAHP480
Db 492 D---PPIHPD---PCCILPIQRYVGLPWLLEASVVIITILSWVGHVKQALISGQCAAI545
Q8 481 PPVHSHNPVTOAREGNLP---LIIT---APALAAVLAALAAVGAAYVVRGPRAMAA533
Db 546 TIATQTTHTFTQHPQVTVTPAVLLEIPQSDPTFPSSILFWVPPNPGVPLVAGPRPSAL605
Q9 534 AQHQDQ539
Db 606 SOGRGO611

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RESULT 4

JC1282

insulin-like growth factor binding protein acid labile chain precursor rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 40 #exp-1993 #text_change 21-Jul-2000

C:Accession: JC1282

E:Pat. 5,710,847; Baxter, R.C.

Biochem. Biophys. Res. Commun. 188, 304-309, 1992

#:Title: Molecular cloning of the acid labile subunit of the rat insulin like growth factor

#:Reference number: JC1282; MUID:93038676

#:Accession: JC1282

A:Molecule type: mRNA

A:Residues: 1-603 (EAL)

A:Cross-references: CR:516785; MID:9358902; PDB:AAB2779.2; PID:95795944

A:Experimental source: liver

A:Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205

C:Superfamily: leucine rich alpha 2 glycoprotein repeat homology

E:1-27/Domain, signal sequence #status predicted #SIG>

E:28-603/Product: insulin like growth factor binding protein, acid labile chain #status

E:267-259/Domain: leucine rich alpha 2 glycoprotein repeat homology #SIG>

A:Residues: 1-1025 <HOL>
 A:Cross-references: PMD:AF074640; NID:q4151258; PID:q4151259; PIDN:AA04345.1
 C:Genetics:
 A:Gene: SL12

Query Match 7.4%; Score 241; DB 2; Length 1025;
 Best Local Similarity 24.8%; Pred. No. 9.8e-06;
 Matches 89; Conservative 42; Mismatches 122; Indels 128; Gaps 13;
 QY 24 CPSQSQSQPQVETARQGTTPRQVPPVTCVYVFENGITMLDASSFAGLPGQLQLDL 83
 DB 223 CPSEKTELD-XXVCSNKGLKVLPGCTPKQVTELYLDGNGQPTLV-FKLSNVKRLTLDL 280
 QY 84 SQNGIASL-----LPRLLLDLSHNSLIALEPGILDTANVFALRLAGLGLQQLDESLF 137
 DB 281 SNKRISLTSNQXFSNNTOILLISYNLRCLPPRTFD-----GLKSL----- 323
 QY 138 SRLKRLHLDIVSNQLEKVPVIRGLGLIKRLKAGNTRIKLAGRFEDLAGLAALQELDVS 197
 DB 424 -RLLSLGNDS-----VVP----- 337

QY 198 NUSLQALPGLSGLPRLMLAAANPNQVPLSWPGPWWRESIVILASPEETRCHEPP 257
 DB 338 ---EGAFNLSA---LSHIAIGANPIVGTNMGWISDWVKSFY--KEPCTAKCAAPG 386
 QY 258 KNAGRLLELDVAFVCPATTITTAIVPTTPVPRPTALSSSLAPTTLWLSPTAPATEAPSP 317
 DB 387 EMADKILLITPSKKFTQ-----GPMQITTOAKNCPCLSN 421
 QY 418 PSTAPPTVGVPP-----GQVQVCP-----PSTCIINGTCHL--GTBHHIACL 356
 DB 422 PKNWTGTONNPVRYRGTCPGKQKQDVPDHAGTINPCKHGKGCHLKEGENAGFWCT 481
 QY 457 CPKCFGLCYCE 367
 DB 482 CADGFEENCE 492

RESULT 15

A34901

lysine carboxypeptidase (887.4.4.17.3) 83K chain - human

C:Species: Homo sapiens (man)

C:Date: 20-Jul-1990 #sequence_revision 20 Jul 1990 #text_change 05-Nov-1999

C:Accession: A34901

R:Tan, F.; Weerasinghe, D.K.; Skidgel, P.A.; Tamai, H.; Kaul, P.K.; Reinson, I.B.; Schi

J. Biol. Chem. 265, 13-19, 1990

A:Title: The deduced protein sequence of the human carboxypeptidase N high molecular wei

Reference number: A34901; MUID:90094186

Accession: A34901

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-536 <TAN>

A:Cross-references: GR:J05158; NID:q179935; PIDN:AAA51921.1; PID:q179936

C:Genetics:

A:Gene: GDH:ACHP

A:Cross-references: GDB:127893

A:Map position: 6q25.3-6q26

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

C:Keywords: hydrolase; metallo carboxypeptidase

F:77-100/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP1>

F:101-124/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP2>

F:125-148/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP3>

F:149-172/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP4>

F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LEP5>

F:197-220/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP6>

F:221-244/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP7>

F:245-268/Domain: leucine rich alpha-2-glycoprotein repeat homology <LEP8>

F:269-292/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LEP9>

F:293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LEP10>

F:317-340/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LEP11>

F:341-364/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LEP12>

Query Match 7.1%; Score 222.5; DB 2; Length 536;
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 QY 25 PSQSQSQPQVETARQGTTPRQVPPVTCVYVFENGITMLDASSFAGLPGQLQLDL 84
 DB 2 PMQCTGF-VQVPCSDPLATVPLIPYENIIPVTSPTTETPRATCCPHRTKVVFL 60
 QY 85 QNOIASLR-----LPRLLLDLSHNSLIALEPGILDTANVFALRLAGL-----LQQLDEG 135
 DB 61 DTQLCCQFRPDAFGGLPRLDELEVGSSEFINISINIF--SNLISLCKLTINENMLEALPEG 118
 QY 136 LLSPLNHLHDIVSNQLEKVPV-VVIRGLGLIKRLKAGNTRIKLAGRFEDLAGLAALQEL 194
 DB 119 LFQHLAALESILHQNLQALPRLFPQPIHFKTINAGNI-LAQDPEEPHPISTQLG 177
 QY 195 DVSNI SIQALPGDISGPPRL 215
 DB 178 KLSNNALSGLP---QGVFQKL 195

Search completed: September 17, 2002, 09:53:44
 Job time: 44.0 sec



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 FT REPEAT 166


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FT REPEAT 505 530 LRR 20.
FT CARBOHYD 64 64 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 85 85 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 96 96 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 368 368 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 515 515 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 580 580 N-LINKED (GLCNAC) (POTENTIAL)
SQ SEQUENCE 605 AA: 66034 MW: 66562A23CB918FC CRC64,

Query Match 9.66; Score 402; DP 1; Length 605;
Best Local Similarity 25.66; Prod No. 15019;
Matches 98; Conservative 40; Mismatches 38; Indels 40; Gaps 11.

QY 7 LLLPLLLL LALG... PRVGS... QPSGSGSQSPQ-----IVGLAKRGHT 45
DB 8 LALLLLSWALGPPSLGSGAGPSTGEARGPACPAACVCSYLALDELVSFSSKRLR 67
QY 16 VPDVPTFTVGLVYFNGTMTLDASSEACI PCLGL LPLSGRCALASLSEFPLI... 98
DB 68 LFDGVPGGTQALWLDGNLSSVPPAFAFONLSSGLFNLGGGGLSLR-PQALGLLENLCH 126
QY 99 LQLSHRLHLEFGILDTANVEALSLAGL... LQQLRRLGFLSEFNFHILFVLSNGLER 155
DB 127 LHLERNQLRSLALGTF--AHTFALASGLSNRNF SPLDGLFEGLSGLDLNLCWNSLAV 184
QY 156 VP-PVITGLRGITLFLACNTFTALPPEDLAGLAALGELVSNLSGLAPRHSLSCHTPP 214
DB 185 LPDAFPGGLGSGSLPELVLAGN-PLAYLQALFSLGFLAPLDELSSRNALPAIKANFVQLPR 243
QY 215 LRLIAAARNPNCVPLSNFEG---PWVPESHVTLA 245
DB 244 LQKLYLDNI IAAVAPCAELGLKALRWLDLSHNVVA 279

RESULT 3
GAC1_HUMAN
ID GAC1_HUMAN STANDARD; PRT; 713 AA.
AC Q75325;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glioma amplified on chromosome 1 protein precursor
GN GAC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homin.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glial tumor;
PX MEDLINE=98324709; PubMed 9562332;
RA Malfroy B., Almeida A., Zhu X.X., Vogt N., Tyagi P., Muleris M.,
RA Dutrillaux A.-M., Dutrillaux B., Foss B., Hanash S.;
RT "GAC1, a new member of the leucine-rich repeat superfamily on
RT chromosome band 1q32.1, is amplified and over-expressed in malignant
RT gliomas."
RL Oncogene 16:3667-3676(1998)
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- TISSUE SPECIFICITY: OVERAMPLIFIED IN MAJORITANT GLIOMAS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
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or send an email to license@isb-sib.ch)).
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DB EMBL: AF030435; AAC30792 1; -

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DR MM: 605492; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00560; LRR_10.
DR Pfam: PF01453; LRR_T1.
DR Pfam: PF01452; LRR_T2.
DR Pfam: PF00319; LRR_PCHPPT.
DR SMART: SM00408; IGG2; 1.
DR SMART: SM00470; LRR; 6.
DR SMART: SM00082; LPPCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 2.
KW Immunoglobulin domain, Transmembrane, Glycoprotein, Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 18
FT CHAIN 19 713
FT L-MAIN 19 630
FT TRANSMEM 631 651
FT DOMAIN 652 713
FT REPEAT 92 115
FT REPEAT 116 139
FT REPEAT 140 163
FT REPEAT 165 187
FT REPEAT 188 211
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FT REPEAT 236 259
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FT REPEAT 309 333
FT REPEAT 334 357
FT REPEAT 359 385
FT DOMAIN 438 504
FT DISULFID 445 497
FT CARBOHYD 94 94
FT CARBOHYD 381 381
FT CARBOHYD 555 555
FT CARBOHYD 583 583
SQ SEQUENCE 713 AA: 78798 MW: 65809PA24069496 QRC64;

Query Match 9.66; Score 282.5; DP 1; Length 713;
Best Local Similarity 22.66; Prod No. 2619;
Matches 176; Conservative 66; Mismatches 255; Indels 223; Gaps 27;

QY 7 LLLPLLLLALG-----PGVGSQSGSQS-----QPSVFCIARQSTTV 46
DB 4 LVAPLLLAWAGATAAVFVFWVHPVCPQCACQIRPWYTPRSSYFEATVDCNLFLLAV 63
QY 47 PRDVP-----PQIVGLV 58
DB 64 PPAIPAPASLHILGSSNLSVPMVLSLQYLANLELLSSQNSFSDAPDCHPAIPOLLSLR 123
QY 59 VEDEITMLKASFASTGICLIPRSGRT ---ASLFELELLLSLSRLALE-- 110
DB 124 LELNGITLTHREFACTASTQELVYRHNQVYFAPFAFSCENIPIELNSL LPAIDSP 183
QY 111 -----PQILD-----PANYVALKACLOGLQGLSGLSKNLHLD 147
DB 184 WFMELPNIFITMTGKNKVDATIMNPFELANFSLVLAMNRIPIFSQYALFELQSLES 243
QY 148 VSDQLRVP-----PVR----- 161
DB 244 FYRQIAKVPSPKALFQVGLKFFLIQRANPLQSGVDFDPAANRILKPLGLNNMELVSLR 303
QY 1+2 -----GLRGLFELGALNIPFAQLPPELALALAGQLLVNLSLQALPDLSCFLPPLRL 217
DB 304 FALVNIPELFTKDTNNPRLSFTHPPAFPHLPQMETLIMNNALSAIHCQTVESIPNIQF 363

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QY 218 TAAAPNPNVCPDLSWFGPWWPESHVTLASPEFTPCHEFPKKNAGRLLELLDYADFQCPAT 277
 DB 364 VGLRKNPTEKLCVLPWAN--AAGSPVFEIRPQSTLTAPPPHLLAPLVFVPPFPEM-----416
 QY 278 TTTATVPTTRVREFTALSSSLAPTWSLPTAFATEAPSPPTAPPTVGPVQPODPCPPS 337
 DB 417 -FDHCLPLISPRSPPSLQVSGESMVLGCRALRAIAEPPEIYVWVTPAGLRLETP-----467
 QY 338 TGLNGTCTCHLCTPHILAC-LPPECF-----TGLY-CFSPQ-----369
 DB 468 -----AHACRR-----FVTPPELTFLPKVTAHEAGSLYTCVALNVLGALTKTVSVVVVK 516
 QY 370 -----MGQCTRPSPDPVTP-----PPPSITLGTPEVSPISLRVGLGPPYLQSSS 413
 DB 517 ALLQPGRGQGLRLRVGTFHYTHLLSWVTPPTNTVSTNLTWSSASLEG--GGAT 570
 QY 414 VQVPSIPLTYPMI SQPKPIVTLPI PASIAPVYVTVQIPPNATYSVVMVLTGPGVPTPPE 473
 DB 571 -----ALRLPRGTHSYNITRLLOATEYWACL-----OV 599
 QY 474 AGGEAHTPPA --VHSNHPVTOAPEGNLPLITA-PALAAVILAA-LAAVGAAYCVPPG- 527
 DB 600 AFADAHTQLACVWATKREATSCHALGRPLGLTALALAVILLIILAAGLAHLGTGQPKGV 559
 QY 528 ---PAMAAAGCFKGVGSG-----ATTELETVKVFLEIPIKALITGGGGA:PSNSPFEVIL 588
 DB 660 GGRPPIPPAWAFWGSAPSVPVVSAPVLT-----PWNPKPK-----IPRSSEGETIL 706

RESULT 4
 GPHA_HUMAN
 ID GPHA_HUMAN STANDARD: PRT: 626 AA.
 AC P07359;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Platelet glycoprotein Ib alpha chain precursor (GP-IR alpha) (GP1RA)
 DE (CD42B-alpha) (CD42b) [Contains: Glycocalicin].
 GN GPIBA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE
 RX MEDLINE=87289655; PubMed=400000;
 RA Loper T.A., Cheng S.W., Fujikawa K., Nagasawa F.S., Papayannopoulou T.,
 Roth G.J.;
 RA "Cloning of the alpha chain of human platelet glycoprotein Ib: a
 transmembrane protein with homology to leucine-rich alpha 2-
 glycoprotein.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5615-5619(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84025874; PubMed=2845078;
 RA Weiser R.H., Kieffer N., Wicki A.N., Clementson K.J.;
 RT "Structure of the human blood platelet membrane glycoprotein Ib alpha
 gene.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987)
 RN [3]
 RP Biochem Biophys Res Commun 156:389-395(1988).
 RN [4]
 RP SEQUENCE OF 17-315.
 RX MEDLINE=87289654; PubMed=3427309;
 RA Tiliari K., Takio K., Handa M., Ruggeri Z.M.;
 RT "Amino acid sequence of the von Willebrand factor-binding domain of
 platelet membrane glycoprotein Ib.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987)
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=91301149; PubMed=2070794;
 RA Hess D., Schallier J., Rickli F.E., Clementson K.J.;
 RT "Identification of the disulfide bonds in human platelet
 glycoprotein.";
 RT Eur. J. Biochem 199:389-394(1991)

EN [5]
 RP VARIANT SIBA.
 EX MEDLINE=92255598; PubMed=1586750;
 RA Murata M., Furuhata K., Ishida F., Russell S.R., Ware J.,
 Ruggeri Z.M.;
 RT "Genetic and structural characterization of an amino acid dimorphism
 in glycoprotein Ib alpha involved in platelet transfusion
 refractoriness.";
 RT Blood 79:3096-3099(1992).
 EN [6]
 RP VARIANT BSS PHE-73.
 EX MEDLINE=92110577; PubMed=1730088;
 RA Miller J.L., Lyle V.A., Cunningham D.;
 RT "Mutation of leucine-57 to phenylalanine in a platelet glycoprotein
 Ib alpha leucine tandem repeat occurring in patients with an
 autosomal dominant variant of Bernard-Soulier disease.";
 RT Blood 79:439-447(1992).
 EN [7]
 RP VARIANT BSS VAL-172.
 EX MEDLINE=93388851; PubMed=7690774;
 RA Ware J., Russell S.P., Marchese P., Murata M., Mazzucato M.,
 de Marco L., Ruggeri Z.M.;
 RT "Point mutation in a leucine rich repeat of platelet glycoprotein Ib
 alpha resulting in the Bernard-Soulier syndrome.";
 RT J. Clin. Invest. 92:1213-1220(1993).
 EN [8]
 RP VARIANT BSS SEP-225.
 EX MEDLINE=95118882; PubMed=7819107;
 RA Sinsek S., Norris P., Lozano M., Pico M., von Dem Borne A.F.G.K.,
 Ribera A., Gallardo D.;
 RT "Cys209 Ser mutation in the platelet membrane glycoprotein Ib alpha
 gene is associated with Bernard-Soulier syndrome.";
 RT Br. J. Haematol. 88:839-844(1994).
 EN [9]
 RP VARIANT PSEUDO-VWD VAL-249.
 EX MEDLINE=91271273; PubMed=2052556;
 RA Miller J.L., Cunningham D., Lyle V.A., Finch C.N.;
 RT "Mutation in the gene encoding the alpha chain of platelet
 glycoprotein Ib in platelet-type von Willebrand disease.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:4761-4765(1991).
 EN [10]
 RP VARIANT PSEUDO-VWD VAL-249.
 EX MEDLINE=95253059; PubMed=8486780;
 RA Murata M., Russell S.R., Ruggeri Z.M., Ware J.;
 RT "Expression of the phenotypic abnormality of platelet-type von
 Willebrand disease in a recombinant glycoprotein Ib alpha fragment.";
 RT J. Clin. Invest. 91:2133-2137(1993).
 EN [11]
 RP VARIANT PSEUDO-VWD VAL-255.
 EX MEDLINE=93214031; PubMed=8384898;
 RA Russell S.P., Roth G.J.;
 RT "Pseudo-von Willebrand disease: a mutation in the platelet
 glycoprotein Ib alpha gene associated with a hyperactive surface
 receptor.";
 RT Blood 81:1787-1791(1993).
 EN [12]
 RP VARIANT BSS LEU-195 DEL.
 EX MEDLINE=95178321; PubMed=7873390;
 RA de la Salle C., Paas M.-J., Lanza F., Schwartz A., Hanau D.,
 Chevalier J., Gacher C., Briquel M.-E., Cazenave J.-P.;
 RT "A three-base deletion removing a leucine residue in a leucine-rich
 repeat of platelet glycoprotein Ib alpha associated with a variant of
 Bernard-Soulier syndrome (Nancy 1).";
 RT Br. J. Haematol. 88:389-396(1995).
 EN [13]
 RP FUNCTION: gp-IR, A SURFACE MEMBRANE PROTEIN OF PLATELETS,
 PARTICIPATES IN THE FORMATION OF PLATELET PLUGS BY BINDING TO VON
 WILLEBRAND FACTOR, WHICH IS ALREADY BOUND TO THE SUBENDOTHELIUM.
 CC -1- SUBUNIT: GP-IB ALPHA AND BETA ARE DISULFIDE LINKED. GP-IX IS
 CC COMPLEXED WITH THE GP-IR HETEROIMER VIA A NON COVALENT LINKAGE.
 CC -1- SURFICIAL LOCATION: Type I membrane protein.
 CC -1- PTM: GLYCOPOLYMER, WHICH IS APPROXIMATELY COEXTENSIVE WITH THE
 CC EXTRACELLULAR PART OF THE MOLECULE, IS CLEAVED OFF BY CALPAIN
 CC DURING PLATELET LYSIS.

DB 115 NQLVFLVSWLGGKALGHIDLSNBRUKPPGGLANFTLLKTLTGDCNGZETILPOLLER 174
 QY 162 GIPGTRPLRIACN-----TPITQIPPERATGAAALQRLVSN 198
 DB 175 GPQLQRIHLHFNKNKIQVIRKDLILPQPLPYPIFNENKLAFAVAAGAPGGLQGLLMLDLSN 234
 QY 195 LSLQALFQ-----ELSSGFPEPFLAFAAFNPNVCPISWFGDPWAVES 241
 DB 235 RELASVPEGLWASLQVHWLWMLWCHFLISS-----NWFLTGLSLSCVFWLWZLA 247
 QY 242 HVTLASPEETROCHFFPKRAGLELL 265
 DB 283 ERMFESQNIPEACGLFAVKGQVILL 306

RESULT 11
 GPV_HUMAN STANDARD: PPT: 560 AA
 ID GPV_HUMAN
 AC 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Platelet glycoprotein V precursor (GPV) (CD42b).
 GN GP5.
 OS Homo sapiens (Human)
 OC Eukaryota, Metazoa, Chordata, Craniota, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 OX NCBI_TaxID=9606.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=93391348; PubMed=7690959;
 RA Hickoy M.J., Hagen P.S., Yagi M., Roth G.J.;
 FT "Human labeled glycoprotein V: characterization of the polypeptide
 RT and the related Ib-V-IX receptor system of adhesive, leucine-rich
 RT glycoproteins.";
 PI Proc Natl Acad Sci U S A 90:8307-8311(1993)
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Platelet;
 RX MEDLINE=94012616; PubMed=8407908;
 RA Lanza F., Morales M., de la Silla C., Carrasque I.P., Clementson K.J.,
 RA Shimomura T., Phillips D.P.;
 FT "Cloning and characterization of the gene encoding the human platelet
 RT glycoprotein V. A member of the leucine-rich glycoprotein family
 RT cleaved during thrombin induced platelet activation";
 RL J. Biol. Chem 268:20801-20807(1993)
 RN [3]
 RP PARTIAL SEQUENCE.
 RC TISSUE=platelet;
 RX MEDLINE=9427204; PubMed=2500000;
 RA Shimomura T., Fujimura K., Maehana S., Takemoto M., Oda K.,
 RA Fujimoto T., Oyama F., Suzuki M., Teihara Tanaka K., Titani K.,
 RA Kuramoto A.;
 FT "Purification and characterization of human platelet
 RT glycoprotein V: the amino acid sequence contains leucine-rich
 RT repeat-like modules as in glycoprotein Ib.";
 RL Blood 75:2449-2458(1990)
 RN [4]
 RP PARTIAL SEQUENCE.
 RC TISSUE=platelet;
 RX MEDLINE=9531255; PubMed=2572284;
 PA Pethica I., Church T.A., McMullen B.A., Williams S.A.;
 FT "Human platelet glycoprotein V: a surface leucine-rich glycoprotein
 RT related to adhesion.";
 RL Biochem. Biophys. Res. Commun. 170:153-161(1990)
 CC -!- FUNCTION: THE GPIB-V-IX COMPLEX FUNCTIONS AS THE VON WILLEBRAND
 CC FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT
 CC PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO
 CC INJURED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A
 CC CRITICAL INITIATING EVENT IN HEMOSTASIS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: PLATELETS AND MEGAKARYOCYTES.
 CC -!- PTM: THE N-TERMINUS IS BLOCKED.
 CC -!- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
 CC THIS SWISS PRO entry is copyrighted. It is prepared through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC send an email to license@isb.slb.ch).
 CC EMBL: L11238; AAA03069.1; -;
 CC EMBL: Z24391; CAAG9637.1; -;
 CC HSSP: P16473; 1XDM.
 CC MIM: 173511; -;
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR000483; LRR_Cterm.
 CC InterPro: IPR000472; LRR_Nterm.
 CC InterPro: IPR003592; LRR_Out.
 CC InterPro: IPR003591; LRR_Typ.
 CC Pfam: PF00560; LRR; 14.
 CC Pfam: PF01463; LRRCT; 1.
 CC PRINTS: PR00019; DEBRICHRPT.
 CC SMART: SM00370; LRR; 1.
 CC SMART: SM00042; LRRCT; 1.
 CC SMART: SM00013; LRRNT; 1.
 CC SMART: SM00369; LRR_TYP; 9.
 KW Platelet, Transmembrane, Glycoprotein, Blood coagulation;
 KW Repeat; Leucine-rich repeat; Cell adhesion; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 560
 FT DOMAIN 17 523
 FT TRANSHEM 524 544
 FT TRANSHEM 545 553
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 FT REPEAT 11690 11713
 FT REPEAT 11714 11737
 FT REPEAT 11738 11761
 FT REPEAT 11762 11785
 FT REPEAT 11786 11809
 FT REPEAT 11810 11833
 FT REPEAT 11834 11857
 FT REPEAT 11858 11881
 FT REPEAT 11882 11905
 FT REPEAT 11906 11929
 FT REPEAT 11930 11953
 FT REPEAT 11954 11977
 FT REPEAT 11978 12001
 FT REPEAT 12002 12025
 FT REPEAT 12026 12049
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 FT REPEAT 12506 12529
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 FT REPEAT 12578 12601
 FT REPEAT 12602 12625
 FT REPEAT 12626 12649
 FT REPEAT 12650 12673
 FT REPEAT 12674 12697
 FT REPEAT 12698 12721
 FT REPEAT 12722 12745
 FT REPEAT 12746 12769
 FT REPEAT 12770 12793
 FT REPEAT 12794 12817
 FT REPEAT 12818 12841
 FT REPEAT 12842 12865
 FT REPEAT 12866 12889
 FT REPEAT 12890 12913
 FT REPEAT 12914 12937
 FT REPEAT 12938 12961
 FT REPEAT 12962 12985
 FT REPEAT 12986 13009
 FT REPEAT 13010 13033
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 FT REPEAT 13058 13081
 FT REPEAT 13082 13105
 FT REPEAT 13106 13129
 FT REPEAT 13130 13153
 FT REPEAT 13154 13177
 FT REPEAT 13178 13201
 FT REPEAT 13202 13225
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 FT REPEAT 13250 13273
 FT REPEAT 13274 13297
 FT REPEAT 13298 13321
 FT REPEAT 13322 13345
 FT REPEAT 13346 13369
 FT REPEAT 13370 13393
 FT REPEAT 13394 13417
 FT REPEAT 13418 13441
 FT REPEAT 13442 13465
 FT REPEAT 13466 13489
 FT REPEAT 13490 13513
 FT REPEAT 13514 13537
 FT REPEAT 13538 13561
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 FT REPEAT 13586 13609
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 FT REPEAT 13634 13657
 FT REPEAT 13658 13681
 FT REPEAT 13682 13705
 FT REPEAT 13706 13729
 FT REPEAT 13730 13753
 FT REPEAT 13754 13777
 FT REPEAT 13778 13801
 FT REPEAT 13802 13825
 FT REPEAT 13826 13849
 FT REPEAT 13850 13873
 FT REPEAT 13874 13897
 FT REPEAT 13898 13921
 FT REPEAT 13922 13945
 FT REPEAT 13946 13969
 FT REPEAT 13970 13993
 FT REPEAT 13994 14017
 FT REPEAT 14018 140

QY 57 LVVFNVTMTDASSPACHPQVTHISNGY ---AST---PPIPIIDISSENIHLP 110
 DB 127 LFDHRAHKGQDPRKQKWHQAFACNCHDFEAFASFTNFRKLELSSNNHILHF 186
 QY 111 PCHLT-ANVVALRAGLGLQLHGERI-----ESRLNLD 145
 DB 167 KCHICANAKTPEHHSNPLVSLGSLNLCALTELQSHNHSIAPGADRLFNSS 246
 QY 146 LDVS-----DNQIFVPPVING----- 162
 DB 247 LLEKHHALFSALEPSHRETLTFENFHALPEVTFPMPCNQFTWNTQETFLP 306
 QY 163 ---LGLTKRLACNT---KLAQLRPDLAALAEADV----- 196
 DB 307 AAAPFNLSRGKYLGVHLSPLKSAIPGAFGLGELAVLHNSGLTALPGLGLGKLR 366
 QY 147 -----SNLS-----LQALPCDLSGLFPLRLAAAPNFV 229
 DB 367 QVSLRKNKRALPRALFNLSLVSGLDQNLLELLGLGVFALPKLHVLLCHNSWKD 426
 QY 229 CHLSWFGVWVHSHVTLASDFE-TPHPPKPNACRLIIPIVDAGCPATTTATVPTP 287
 DB 427 GGLGFETGLWRO HGLGVGHEEPKACGCAHAGLPIWALPGTARCPG-----PRGP 478
 QY 288 PVVREPTALSSLAPTWLSPTAPATEAPSPSTAPTVGP 327
 DB 479 P-PRPADSS-----RAPVHPALAPNSSEP 503
 RESULT 12
 ID CBP8_HUMAN STANDARD: PRT: 536 AA
 AC P22792;
 DT 01-AUG-1991 (rel. 19, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DE Carboxypeptidase R 83 kDa chain (Carboxypeptidase N regulatory
 subunit) (Fragment).
 CN CPB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid:6606;
 FN
 RP TISSUE: Liver;
 RC SEQUENCE FROM N.A.
 RX MEDLINE 90094486; PubMed 2474615;
 TA Tan F., Weerasinghe D.K., Skidgel R.A., Tamei H., Kaul R.K.,
 Robinson L.B., Schilling J.W., Erdoes E.G.;
 "The deduced protein sequence of the human carboxypeptidase N high
 molecular weight subunit reveals the presence of leucine rich tandem
 repeats".
 RL J. Biol. Chem. 265:13-19(1990).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE 88309120; PubMed 3408501;
 RA Skidgel R.A., Bonsoff C.D., Schilling J.W., Weerasinghe D.K.,
 Erdoes E.G.;
 "Amino acid sequence of the N-terminus and selected tryptic peptides
 of the active subunit of human plasma carboxypeptidase N: comparison
 with other carboxypeptidases".
 RL Biochem. Biophys. Res. Commun. 154:1323-1329(1988).
 CC FUNCTION: THE 83 KDA SUBUNIT BINDS AND STABILIZES THE CATALYTIC
 SUBUNIT AT 47 DEGREES CELSIUS AND KEEPS IT IN CIRCULATION. UNDER
 SOME CIRCUMSTANCES IT MAY BE AN ALLOSTERIC MODIFIER OF THE
 CATALYTIC SUBUNIT.
 CC SUBUNIT: TETRAMER OF TWO CATALYTIC CHAINS AND TWO GLYCOSYLATED
 INACTIVE CHAINS.
 CC SUBCELLULAR LOCATION: Secreted.
 CC PTM: O-GLYCOSYLATED IN THE SER/THR-RICH REGION (POTENTIAL).
 CC PTM: WHETHER OR NOT ANY CYS RESIDUES PARTICIPATE IN INTRACHAIN
 BONDS IS UNKNOWN, BUT THEY DO NOT FORM INTERCHAIN DISULFIDE BONDS
 WITH THE 50 KDA CATALYTIC SUBUNIT.

CC DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOT CONSIDERED TO BE
 COMPATIBLE WITH LIFE.
 CC SIMILARITY: CONTAINS 13 LEUCINE RICH REPEATS (LRR).
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 or send an email to license@sib-sib.ch.
 DB EMBL: J05158; AAA51921.1; --
 DB PIR: A34901; A34901;
 DB MIM: 603104;
 DB InterPro: IPR001611; LRR.
 DB InterPro: IPR003372; LRR_NTerm.
 DB InterPro: IPR003591; LRR_Typ.
 DB Pfam: PF00560; LRR_11;
 DB SMART: SM00013; LRRNT; 1.
 DB SMART: SM00359; LRR_Typ; 10.
 KW Repeat; leucine-rich repeat; Glycoprotein.
 FT NON_TER 1
 FT REPEAT 51 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 123 146 LRR 4.
 FT REPEAT 148 170 LRR 5.
 FT REPEAT 171 194 LRR 6.
 FT REPEAT 196 218 LRR 7.
 FT REPEAT 220 242 LRR 8.
 FT REPEAT 243 266 LRR 9.
 FT REPEAT 268 290 LRR 10.
 FT REPEAT 291 314 LRR 11.
 FT REPEAT 316 338 LRR 12.
 FT REPEAT 339 362 LRR 13.
 FT DOMAIN 359 375 SER/THR-RICH.
 FT CARBOHYD 53 53 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLNAC); (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLNAC); (POTENTIAL).
 SQ SEQUENCE 536 AA; 58649 MW; D524D11243092A6 CR664;
 Query Match 7.1%; Score 222.5; DB 1; Length 536;
 Best Local Similarity 34.9%; Pred. No. 4.7e-06;
 Match 76; Conservation 27; Misc. other 87; Table 17; Gap 7;
 QY 25 PSCQCSQPTVCTARQGTIVPRVDPVTVVYVFNGLTMDLASSFALGLQLDLIS 84
 DB 2 PMSQVTF-VQEVFVSQFPAIVDIPFVTKNIPVFSFTFTFTRAPGNSNITKVVFL 60
 QY 85 QNQCASIF ---LTLTSHNCTALPVALTITATVVALPIADG---LQIDRQ 135
 DB 61 DTQLCQPPAPAGSIPRIPIPIVTVSSPNSINIP-SNITSLKLTLPNNMLALPQ 118
 QY 136 LFSPLNHLDDVSDNGLEPVP-FVHGLGCTRLACNTRIAQLRPDLAALQEL 194
 DB 119 LFDHRAHKGQDPRKQKWHQAFACNCHDFEAFASFTNFRKLELSSNNHILHF 177
 QY 195 DVSNLSLQALPCDLSGLEPL 215
 DB 178 KLSNNALSGLP---GVVFGKL 195
 RESULT 13
 ID PLIB_AGBL STANDARD: PRT: 331 AA.
 AC Q93233;

30-MAY-2000 (rel 39, Created)
 01-MAY-2000 (rel 39, Last sequence update)
 01-MAR-2002 (rel 41, Last annotation update)
 DE Phospholipase A2 inhibitor subunit A precursor (PII-PI)
 OS Akkistrodon blomhoffii sinensis (Chinese manushi) (Glycidias
 blomhoffii sinensis)
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 Lepidosteiformes, Scombridae, Scombrinae, Serpentes, Colubridae,
 Viperidae, Crotalinae, Atractaspidinae
 NCBI_TaxID=31147;
 RN [1]
 PP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 59-87; 94-105, 165-173,
 177-195; 204-219; 226-242; 305-313 AND 317-330
 RC TISSUE=Liver;
 RX MEDLINE=98344034; PubMed=9677367;
 PA Okamura K., Ohkura N., Inoue S., Ikeda K., Hayashi K.;
 PT "A novel phospholipase A2 inhibitor with leucine rich repeats from the
 RT blood plasma of Akkistrodon blomhoffii sinensis. Sequence homologies
 RT with human leucine-rich alpha2-glycoprotein";
 PI J. Biol. Chem. 273:19469-19475(1998).
 CC [2]
 CC SEQUENCE OF 24-53, CHARACTERIZATION, AND FUNCTION.
 CC TISSUE=Plasma;
 CC MEDLINE=97361946; PubMed=9230137;
 CC Okura N., Okhata H., Inoue S., Ikeda K., Hayashi K.;
 CC "Purification and characterization of three distinct types of
 CC phospholipase A2 inhibitors from the blood plasma of the Chinese
 CC manushi, Akkistrodon blomhoffii sinensis";
 CC Biochem J. 325:527-531(1997)
 CC [3]
 CC FUNCTION: INHIBITS THE ENZYMATIC ACTIVITY OF THE BASIC
 CC PHOSPHOLIPASE A2 (PLA2).
 CC [4]
 CC SUBUNIT: HOMOTRIMER.
 CC [5]
 CC MASS SPECTROMETRY: MW=43857.2; MW EXP=81.9; METHOD=MALDI.
 CC [6]
 CC SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR).
 CC [7]
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 CC or send an email to license@isb-sib.ch)
 CC [8]
 CC EMBL: AB007198; BAA31994.1;
 CC HSSP: P16473; LXUM.
 CC InterPro: IPR001611; LRR
 CC InterPro: IPR000482; LRR_CtorP
 CC InterPro: IPR003582; LRR_Cup
 CC InterPro: IPR003581; LRR_Typ
 CC Pfam: PF00560; LRR_8
 CC Pfam: PF01463; LRRCT; 1.
 CC PRINTS: PR00019; LEPTICHPPT.
 CC SMART: SM00370; LRR_1.
 CC SMART: SM00082; LRRCT_1.
 CC SMART: SM00369; LRR_Typ; 3
 CC Signal, Phospholipase A2 inhibited, Glycophorin-B, E-F-actin,
 CC leucine-rich repeat.
 CC SIGNA: 1 23
 CC CHAIN 24 331 PHOSPHOLIPASE A2 INHIBITOR SUBUNIT B.
 CC REPEAT 78 101 LRR 1.
 CC REPEAT 103 125 LRR 2.
 CC REPEAT 127 149 LRR 3.
 CC REPEAT 150 173 LRR 4.
 CC REPEAT 175 197 LRR 5.
 CC REPEAT 199 221 LRR 6.
 CC REPEAT 223 244 LRR 7.
 CC REPEAT 245 268 LRR 8.
 CC CARBOHYD 35 35 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 125 125 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 232 232 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 271 271 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CONFLICT 45 45 S-L (IN REF. 2)
 CC SEQUENCE 331 AA: 376-1 MW: 43857.204 Da
 CC

Query Match 6.98; Score 215.5, DR 1, Length 331;
 Best local Similarity 26.98; Pos No 7,1e-06;
 Matches 96; Conservative 34; Mismatches 112; Indels 112; Gaps 14;
 57 1 MSSEVFLIPHLLEALGHNVAETSTSEVQGGQIVFNAPELIVLEVPI HIVL 57
 DB 1 MKSSVPSLLIACLVNSLSNYTQ-----QVLYCPP-----TPAPNVIEFVCSNLSL 46
 QY 58 YVFNQ-----ITMIPASSPAGIPHILHLSNQTASL-----PLPRL 97
 DB 47 HETTPATPAFAKMSVETTSVSAEVAEQENENQELHLSNKLKTLFSGILRNLPOLH 106
 QY 98 IIPLSINSLIAPPGHIDIAN-----ITMIPASSPAGIPHILHLSNQTASL-----PLPRL 97
 DB 127 TLELEINLELITFTFNASSLILPLFENALALHLSWETLGEELGLGHHQVKEI 166
 QY 135 --GLFSPLFNHLHLSVSNGLPPV-PPVTPKSLGLRIRPLAGN-----IR 176
 DB 167 FISCPELKELTSLDPLFLPLADFMESGLNLEKLLLESNPLOCVGFTTHHPRKL 226
 QY 177 IACLPDENIAG-----LAATQELDVS-----NLSQALPDGLSCLEPP 213
 DB 227 VLKSSSLINMTHQLLEGEELHLSNQLTMEETVYKISANLSL DISG--- 278
 QY 214 FLPLAAAPHPEWVPLSWPPIWPPFIVIVLASEPTSCHTTTCNAGSEIILVYVAPG 273
 DB 279 -----HWAGCELDRLITWNHRIHLYSKHEIVCASTRFREGDQATSLHKS 228
 QY 274 QP 275
 DB 329 QP 330
 RESULT 14
 CHAD BOVIN STANDARD; PRI; *51 AA.
 ID CHAD BOVIN STANDARD; PRI; *51 AA.
 AC G2792;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 30-MAY-2000 (rel. 49, Last annotation update)
 DE Chondroadherin precursor (Cartilage leucine rich protein) (38 kDa bone
 DE protein).
 DE CHAD.
 GN Bos taurus (Bovine).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Cetartiodactyla, Fuminantia, Pecora, Bovidea;
 OC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 PP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Cartilage;
 EX MEDLINE 94342341, PubMed 8063792,
 PA Reame P.J., Sommarin Y., Beynon P.E., Hinegaard D.;
 FI "The structure of a 36 kDa leucine rich protein (chondro-adherin)
 RT isolated from bovine cartilage";
 RL J. Biol. Chem. 269:21547-21554(1994).
 RN [2]
 RN SEQUENCE OF 25-55 AND 77-97.
 RC TISSUE=Bone;
 RX MEDLINE=95113864; PubMed=7814406;
 PA Ha R., Coulson L., Moyer R., Price P.A.;
 RT "Isolation and molecular cloning of a novel bone phosphoprotein
 RT related in sequence to the cystatin family of thiol protease
 RT inhibitors";
 RL J. Biol. Chem. 270:431-436(1995).
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CC EMBL: U08018; AAA21330.1; -.
CC InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR004591; LRR_Typ.
DR Pfam: PF00560; LRR: 10.
DR Pfam: PF01463; LRRNT: 1.
DR Pfam: PF01462; LRRNT: 1.
DR SMART: SM00082; LPPCT: 1.
DR SMART: SM00013; LRRNT: 1.
DR SMART: SM00369; LRR_Typ: 5.
KW Repeat; Signal
FT SIGNAL: 1 24 CP 23 (IN SOME ISOFORM(S))
FT CHAIN: 25 361 CHONDROGADHERIN.
FT DOMAIN: 25 352 CHONDROGADHERIN, MINIP FORM.
FT REPEAT: 79 317 10 X 24 AA LEUCINE-RICH TANDEM REPEATS.
FT REPEAT: 103 126 1.
FT REPEAT: 127 150 2.
FT REPEAT: 151 174 3.
FT REPEAT: 175 198 4.
FT REPEAT: 199 222 5.
FT REPEAT: 223 246 6.
FT REPEAT: 248 271 7.
FT REPEAT: 272 293 8.
FT REPEAT: 294 317 9.
FT DISULFID: 306 348 10.
FT DISULFID: 308 348 1.
FT CONFLICT: 25 25 C S Y (IN REF. 2).
FT CONFLICT: 29 29 C S W (IN REF. 2).
FT CONFLICT: 31 31 C S H (IN REF. 2).
FT CONFLICT: 40 40 C S L (IN REF. 2).
FT CONFLICT: 52 52 S S R (IN REF. 2).
SQ SEQUENCE 361 AA; 40884 MW; DA/SGRADSDDIER CRC64;

Query Match
Best Local Similarity 6.88; Score 213.5; DB 1; Length 361;
Matches 92; Conserved at, Mismatches 100, Indels 10%, Gaps 12.

QY 7 TLPLILLIATGKVPSPGQVQVETAFQHTVPR-----LVP 61
DB 8 LLSLGLLALIPALAAQDQCHPSDLQHVICHKVGGLQKPKVSEKTKILNIQRNFPV 67
52 -----PTVGVGVYFPRIPMLDASSFACHGLGLLGLSLKSLASLA 92
68 LATNSFRAMPNIVSHQHQCFQFVAGAFQGLKQLYLYLSHNDIVLRAGAFDDITPL 127
93 -----LPRLLI-----LDLSHNSLLA 108
DB 128 TYLYLHNKVTPLPGLLSPLVNLFLQLNNKIPFLPSGAFQAKLPMWLYSENSLS 187
QY 109 LPQTHITANVETPLAQDGLD-----EPLFSPINPHTIVFNGLEFVDF-VTP 164
DB 188 LQPGALD--DVENLAKFYLDNQLSSYPSAALSILRVVEELKLSHNPDKSIDPNAQSF 245
QY 165 GLTPVPLACNPFVACFPEULACAAQLPLVLSNLSQAQLPGLSCLFPLPLAAAPR 224
DB 246 PYLFTIWDINTLRFPSGAFGLVTTKLVHLENNPLHQFSNFP--FDSLETLTNNP 303
QY 225 PNVVPLSWPQHWV-----PSNVTASPEPQ-----CHPT--PKNAP 262
DB 304 WKCTQGLKGLPFWLEKATSPVIAIPASAKFPGQHPHPIIAFPAKPEPKESKAK 600

RESULT 15
ID PRLP_HUMAN STANDARD; PRT; 382 AA.
AC P51888;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01 OCT 1996 (Rel. 34, last sequence update)
DE 01-MAY-2002 (Rel. 41, last annotation update)
DE Prolagin precursor (Proline-arginine rich end leucine rich repeat
DE protein).
GN PRELP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MPTINP-4602653; PubMed=7592739;
RA Bengtsson E., Neame P.J., Heinegaard B., Sommerin Y.
PT "The primary structure of a basic leucine-rich repeat protein, PRELP,
PT found in connective tissues".
PT J. Biol. Chem. 270:25639-25644(1995).
FL [2]
RP SEQUENCE FROM N.A.
RP SPQNFTE FROM N.A.
RX MEDLINE=97127584; PubMed=8954791;
RA Grover J., Chen X.-N., Korenberg J.P., Recklies A.D., Routhley P.J.;
PT "The gene organization, chromosome location, and expression of a
PT 55-kDa matrix protein (PRELP) of human articular cartilage";
RL Genomics 38:109-117(1996).
CC -!- TISSUE SPECIFICITY: CONNECTIVE TISSUE.
CC -!- SIMILARITY: BELONGS TO THE SMALL INTERSTITIAL PROTEOGLYCANS
CC FAMILY.
CC -!- SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LRR).
CC -----
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Query Match 6.78; Score 208.5; DB 1; Length 482;
Best Local Similarity 26.48; Pred. No. 2.1e-05;

QY 472 EACGCHAMTPAVSHNATV TCAAGCNLDLTAATLAAVLAALAAVAAVAFVLE- 526
 DB 603 LGAGHARPEKTHIDRNGRIRVDPICAFG-IPATLEIUSNPIPALR-CAEUPWGRS 660
 QY 527 -----CPAMAAAGQWCVWCAACPLDIFGVVVFETGPKATEGGGALSGRST 577
 DB 661 LQHLFINSIGLEICGCAFSG-IGDGLQSHKQKQIPALP-----ALPSLSOLE 709
 QY 578 V 578
 DB 710 L 710

RESULT 8
 043155 PRELIMINARY: PRT: 660 AA.
 AC 043155
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE KIAA0405 (LIFINP-RICH REPEAT TRANSMEMBRANE PROTEIN PTPT2)
 GN KIAA0405 OR FLRT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Primates; Catarrhini; Hominoidea; Homo
 OX NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN
 RA Ishikawa K., Nakase T., Nakajima D., Seki N., Ohira M., Miyajima N.,
 Tanaka A., Kotani H., Nomura N., Ohara O.,
 KL Submitted (oct-1997) to the EMBL/GenBank/DDBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 20112755; PubMed: 10444449.
 RA Lacy S.E., Konemann C.G., Buzney E.A., Kunkel L.M.:
 RT "Identification of FLRT1, FLRT2, and FLRT3: A Novel Family of
 RT Transmembrane Leucine-Rich Repeat Proteins";
 RL Genomics 62:417-426(1999).
 DR EMBL: AB007865; AAA23701.1;
 DR EMBL: AF164676; AAF28460.1;
 DR InterPro: IPR003461; FN.111.
 DR InterPro: IPR001611; LRR
 DR InterPro: IPR000483; LRR_Gterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR001211; P2_A2.
 DR Pfam: PF00041; In3; 1.
 DR Pfam: PF00560; LRR; 9.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART: SM00370; LRR; 3.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00143; LRRNT; 1.
 DR SMART: SM00369; LRR_TYP; 1.
 DR PROSITE: PS00119; PA2_A21; CHERM_1.
 KW Transmembrane.
 SQ SEQUENCE 660 AA: 74048 MW: 98152383kDPSF778 CPG64;

Query Match 10.2% Score 320, DB 4: Length 660.
 Best Local Similarity 22.4% Pct. Id. 7.4e-15,
 Matches 140; Conservative 97, Mismatches 216, Indels 182, Gaps 23;
 QY 13 LLLALGPGWQ-----GCPSCWVSCAPVFTAPASITVDPVDPVGLVLF----- 60
 DB 20 LLLSLAGYQVSKLLACVSCVCRDR-NFYVYCNERSLTSPPGVTVLYHNHNNQINNA 78
 QY 61 -----ENGLTMDLADSFAGLQGLQL 81
 DB 79 GPFAELHNVQSVHTVYVYGNQLDFPPMNI PKNVVPVHLHGFNNIQTISPAAALQILFLREI 198

QY 82 ELSSQSTANSELF -----KLLLELLCHRLALESS- LSTANVVALEKA GL 127
 DB 139 HLLNLSISTVGVHGAFAREALSKLILFSLKNLSSVWGLFVDFQELKVDENKIAVISM 198
 QY 228 GSGOLD-----EGLVSELRRLHLLVSSRLKEEVVTVLESLKELTEL 169
 DB 199 AFONLSLEPLIVGNLTKNGIAESTSHLTKEEFSIVENSLSHPPDLPETH-LIRL 267
 QY 170 PLAGNDFIADIFDIAAGAAQDILVSHIETGALQDN SGI FDFR PLTAAAPRPPVW 329
 DB 258 YLQSN-QIHHIPIIATPSNLEKIFRIPICNNGEMITGVTHIENIKQIATANNIWFYWC 316
 QY 230 PLSWFGWVWESHVTLASTPEETRCHITPKNAKLELLDYADFGPATTTATVTHPV 289
 DB 317 SKKWTFWKYIDSSI-NVSGFMCGQDFVGRGMVRFNMNI SCF--TITGLGLFDP- 372
 QY 290 VREPTALSSSLAPTSLPTAPATEAPSPSTAPTVGVGPQVQVPPSPINFGTCHLGT 349
 DB 373 -----APST---ASITQPTLS-IPNI-----S 392
 QY 350 PPHIACIQCPGPGHLYCPQSMQCCGPPPPPP-----VPPPPRPSITLIEP 395
 DB 393 RSY-----TPPTTSKLTPIPDWCGREWVTHPISEFQLSIHF 431
 QY 394 VSTPLPVVIGRYTQSSSVQI ESI PLTVSHI SPTKPIVTVPLASIAFY-TVQLRINA 454
 DB 432 VNDISQVSWLSIFVIMAYKLTWKGHSIVG3-----IVQRTVSGRKHLSLVNLEPRS 487
 QY 455 TVSCVYMPDIPGPPVPRGEAA-CSEAHITFA-----VESNHIAVTEAPRGNLILAPA 506
 DB 488 TYRICLVPLDAFYNAVEDTICSEATTHIASVYLNKSGTASSHEQTTSMSGS-PELLAGL 546
 QY 507 LAAVLLAALAAVCAAYC----VRRGR 528
 DB 547 TCGAVIFVAVLLSVFCWMEKEGR 571

RESULT 9
 QY0017 PRELIMINARY: PRT: 792 AA.
 AC QY0017
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE WUGSC-H_GS165L15.2 PROTEIN (FRAGMENT).
 GN WUGSC-H_GS165L15.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Geisel C., Antoniou B., Angel S.:
 RT "The sequence of Homo sapiens BAC clone GS1-165L15.2";
 EL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA Waterston R.:
 DT Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AC005013; AAC79690.1;
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Gterm.
 DR InterPro: IPR000472; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR; 10.
 DR Pfam: PF01463; LRRCT; 1.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00013; LRRNT; 1.
 DR SMART: SM00369; LRR_TYP; 10.
 DR NON_TER 1
 SQ SEQUENCE 792 AA: 86456 MW: 10420484.4EAFERB7C CPG64;


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Db 526 KAETA-----DSYGTTLNQAGNAGMASLPIAGITGGAAVAIVFLVLGAICWVYHOAG 581
QY 522 YCVPRGMAAAAGKQVCPGACPLFEGVAVKPLFPGKATGGGGAALPGSGRCEVPLM 581
Db 582 ELUTRPAYNPGSPFR-----DOYMESOTFKDNSIL 612
QY 582 GEPGGLQ-----SPLIAK 595
Db 613 EIKCPGLQMLPINPYRAK 630

RESULT 11
ID Q9P254 PRELIMINARY; PRT: 662 AA.
AC Q9P254;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE KIAA1469 PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-20277482; PubMed-10819331;
FA Rabea T, Kikano E, Ishikawa K, Hirokawa M, Ohata G;
RT Prediction of the coding sequences of unidentified human
RT genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro.*;
PL DNA Rec. 7:143-150(2000).
DB EMBL: AB040902; BAA95993.1;
DR InterPro: IPR003961; FN_111.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR001211; PLP_A2.
DR Pfam: PF00041; fn3.1
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00370; LRR; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 1.
SQ SEQUENCE 662 AA: 74459 MW: 847000.6844429 GPC64;

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Query Match 9.94, Score 359; DB 4, Length 662;
Best local similarity 22.99; Pred No. 4,6614.
Matches 146, Conservative 97, Mismatches 216, Indels 192, Gaps 27,

QY 2 GSAPVLLDPL-----LLIAGLP- GVAGTSSGTCGSCPGQIVPVYIAGGI 44
Db 5 CIKSTLLTMSAAMSIFLIGTKIGLFGVAPLSVNAKSCPSVCG-(D)HY-NQPHIT 64
QY 45 TVPQWPPVTVIVFVPPNITMIDASSFAGIIG-----NNAGTSTLKNLKVRIYLYHNSLLEPPINLPK 117
Db 64 SIPTGIPGATLLYLQNNQJ-----NNAGTSTLKNLKVRIYLYHNSLLEPPINLPK 117
QY 78 -LQIDLISQNGIASI-----RPPILLIDISNLSL--LALPGLITLITANVAFLPIAGIG 128
Db 118 YKVELHLQNNRTITIDYLSKIPYIEELHLDDNSVASVTEGAFKSNY--LRILFLS 175
QY 129 LQVDEGLSPFNPGLHIVSNQKLPFV-PVIVFIPGLTETFLAGN----- 174

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Db 176 FNHLSTIPWELPTEELNPFSTISSPSLGLISLKLPLVLENNLNHGLHGLKVEF 235
QY 175 -----TRIAGLR-----PDLAG-----LAAIGELHVSLS 200
Db 236 NEVNLTELSLVPSNLTAAPVNLPGTNLELYLYQNEINFEVFNHAFSYLQLYPLDSSNN 295
QY 201 LQALPGDLSLFPPEPLTAAAPNPNVCTVSWPGVWVWVPSHIVTLASDEFTTHCHTFPNA 260
Db 296 LSNLPAGTIFGLLINLIGLILKNPWYVCKMAWPHIWIQSLPVKV-NVPGIMQVAPVVR 354
QY 261 GRILLELDYADFQCPATTTTATVPTTRPVVREPTALSSSLAPTWSLPTADPAEASPEST 320
Db 355 GMAIKDLNAELFDCKDSGIVSTLIQT-----TALPNIVYPAQGWAPVTKQPD----- 403
QY 321 APPTVGVVTPQDGPSTCTNGCTCHLGTTHHLAGLTPFTGLYCESQMGAGTSPSTP 380
Db 404 -----IKNPK-----LTKDR-----OTTCGFS 420
QY 381 VTEPFESTLGTIEFVSPTSIRVNLQPVYQSSVQIESRLTYPNLSGP-IPKRLVTLRLP 439
Db 421 -----RKTITIVKSVTSDTIHLSKKLPMALPTALRLSLWKLCHSPAGSITETIVT----- 471
QY 446 ASGAYIVIVLFINATYSWTVMIIGVGRVVEGFF ACQPAHTTPAVVSHAPVT----- 492
Db 472 GERSEYVTLALDFDSYKVCVMVFMETSHLYLDFETVQVCTETETAPLEMYN PTTILRE 529
QY 493 QARE-----GNLPL--LIAPALAAVLLAAVCAAYCVPRGPMAAA-AAQHKQ 539
Db 530 QEKERYKNIRLIIAAIGGAVALVTLLALIV-CWYVHRNGSLSEFSENGAYSKGR 582

RESULT 12
Q9NZU0 PRELIMINARY; PRT: 649 AA.
ID Q9NZU0;
AC Q9NZU0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE LECICINE-RICH REPEAT TRANSMEMBRANE PROTEIN FLRT3 (DJ581113.1).
GN FLRT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-20112755; PubMed 10644439;
FA Cary S E, Pennison C S, Buehler J A, Forks J H;
RT Identification of FLRT1, FLRT2, and FLRT3; A Novel Family of
RT Transmembrane Leucine-Rich Repeat Proteins.*;
PL Genomics 62:417-426(1999).
DB EMBL: AB040902; BAA95993.1;
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR001211; PLP_A2.
DR Pfam: PF00041; fn3.1.
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00370; LRR; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 1.

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RP SEQUENCE FROM N.A.
 RA Isodai T., Ota T., Hayashi Y., Sugiyama T., Otsuki T., Sasaki Y.,
 RA Nishikawa T., Nishikawa T., Nishikawa S., Arita S., Yoshikawa Y.,
 FA Nakamura Y., Ishii S., Fuzai Y., Saito F., Yamamoto T., Wakatsuki A.,
 RA Nakamura Y., Nakahara K., Masuko Y., Sasaki N.,
 RT "NDO human cDNA sequencing project";
 RL Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027694; BAR5303.1; - PARAR65767107A7A CPO64;
 SQ SEQUENCE 624 AA: 70245 MW: 74132 MW: 37981820407H01C0 CPO64;

Query Match 9.68; Score 299.5; DR 6; Length 677;
 Best Local Similarity 24.28; Pred. No. 2,4e-13;
 Matches 140; Conservative 93; Mismatches 209; Indels 175; Gaps 25;
 22 QVPSGQVQSGQVETATQVTTVPVAVPPTVTVVYFNCITMIDASSPACLP----- 77
 DB 3 KSCPWCRC-TAGFYVYVNRFTISPTIPEDATTIVYLNQCL-----NNAGIPSELKN 55
 78 -----LQLDLSONQIASI-----KPKKLLLLSHNSL- 106
 56 LUKVERIYLYHNSIDREPTNIPKYVRELUHGDNNITPTIYDSLSKIPYLEELHLDNVS 115
 107 -LAIPTCILPTANVALPLACIGGLDEGLFSELPNEHELVSDNGLEK-PAVIVKELP 154
 116 AVSLEGAERGSNY--LRLGLSKWHSI-LWGLPRTIEFLRLKPLISLSSSLAGLEP 173
 165 GLTRPLACN-----TPIAQLP-----PPIAG- 187
 174 SLKPIVLVNTINNHLGKGVFNVLNLTSLSVNSLTAAPVNLPGTINLKYLQUNHI 233
 188 LAAGLLAVNLSGALFGDLSGLTFLRLILAAAPNPNVCTLSWGFV 247
 234 NPVPPNAPSYIPCTYPLMSNNLSNEGGTFEFLPNITQLILNNWYVYVFKWVFGW 243
 238 VPSHVVTIASPPTCHPTFNACPLLELDYADEGCAITITIAVITHEVVRFPALS 297
 294 LQSLPKV-VNAGLGCQAFKVGKMAIKNAELFLCKKISVSEIQLT-----IATP 345
 298 SSLAPTWLSPTAPATAPSPSTAPPTGVPVPGQGPPEPTCINSGTCHLCTHHLACT 357
 346 NIVYAGCGWPAVTKQED-----TNNR-----ITKH----- 374
 358 PRGFTGIVCESOMGCGTPSPPTTPRPPSITIGIFVSPSTLPVGIQVYLOGSSVCLP 417
 375 -----QTTGSPS-----PKTITTVKSVTSPTTHISWKLALPMTALPLS 413
 418 SLPIITYPNI SQP-DRELVTIPEASIAVYVTOI PPNATYSVCMPLGPGVPECEP--A 474
 414 WLKLGHSFAPGSIPTTIVT-----GPFSEYIVTALFPGSPYKVVWVPMETNLYLFTPV 459
 475 GGEAHTPPAVHSHNAPVT-----QAPR-----LAFALAAVLLAALAAVGAAYC 523
 470 CTFETAPILRMN--PTTINRFGKFPKKNPIPLAATIGTAVAIYVIALIAYL-TWV 526
 524 VERGRAMAA AADGKQ 539
 527 HNGSLSPNAYSKP 543

RESULT 15
 Q28256 PRELIMINARY: PRY 677 AA.
 AC Q28256;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE GLYCOPROTEIN 1B.
 OS Canis familiaris (Dog).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
 OX NCBI_TaxID=9615;
 RN 11

RP SEQUENCE FROM N.A.
 EX MEDLINE: 20011007; PubMed 10544923;
 FA Kohn D., Metatsek P.A., Fahs S.A., Wallner D.C., Montgomery P.R.;
 FT "Cloning and expression of canine glycoprotein 1b alpha";
 RL Thromb. Haemost. 82:1327-1333(1999).
 DB EMBL: U19489; AAC14361.1; -
 DB InterPro: IPR001611; IPR;
 DB InterPro: IPR000483; IPR_Cterm.
 DB InterPro: IPR000370; IPR_Rterm.
 DB InterPro: IPR003562; IPR_out.
 DB InterPro: IPR003561; IPR_type.
 DB Pfam: PF01463; JERSCT; 1.
 DB Pfam: PF01462; LERRF; 1.
 DB SMART: SM00370; IPR; 2.
 DB SMART: SM00082; LPECT; 1.
 DB SMART: SM00013; LPPNT; 1.
 DB SMART: SM00359; LRR_type; 3.
 SQ SEQUENCE 677 AA: 74132 MW: 37981820407H01C0 CPO64;

Query Match 9.68; Score 299.5; DR 6; Length 677;
 Best Local Similarity 24.28; Pred. No. 2,4e-13;
 Matches 150; Conservative 90; Mismatches 189; Indels 221; Gaps 26;
 7 LLLPILLILLALPQVQGPESNQSQVQVETAPQCTTPVPRVPPVPTVGLYVFEN----- 52
 DB 3 LLLWLLLLALPQPEPFCEVSVTSQVE-VNCDNRGLKALPPGIPGDTAILHAEPLGA 61
 63 -----GITMIDASSFAGLQGLQILDLSONQIASI-----RPRLL 97
 62 FSTATIGELTFLAQLHDEGSLTGLQVGM LPELLELDVSHKRSKSLSEGRALFALT 119
 98 LLDLHNSLLALPPTIITANVEALPIAGLGLQGLDPCI FSLPLNLDHLDVSDNLERVP 157
 120 TLDASERELVALSEGLD-----GLSHLHLYLSEGRKATLP 156
 158 P-VVIGSLKGLTHPLAGNPLIAGLPPELHAGLAAQLPILVSNLSIALP-----GHSSGLP 212
 157 PLLAPLACLEKLNLAUN-PLLELPFSELEGLDTLYLQGNMIPVPKGFDTLLIPP 215
 213 PLELLAAAPNPNVCDLSWFGPWV-----PSHVTLASPPTPQ-----HP 255
 216 TPLH-----GNWSCTGPIYLAFLWIPUNSNVVIWPCVFAKATTPVINSVPCVWKNV 270
 256 P-----PKNAGPLILLELDYADP-----GCPATTTTATV----- 283
 271 PVHTYCKDCTSPMGQ-----DMYENTDREDEKLPCVEAIPAVVVSFHHKAITHW 326
 284 -----PTTPVPRPTALSSSLAPTWL 405
 327 GLLYTTFATVGHQAYLSLLELTKQCTMPSTLQPMFTTP---EFTTFTTFTT T 392
 406 SPALATAPSPSPSLAPVIVGVVQVQGLSPGSTCINACTHATTHHACTGPGSTGLY 365
 383 TPTTF EFTTFTTFTTFTT TPEPTMPPTLEPT-----TPTTPE----- 424
 366 GFSOMGCTGSPSTVTPDPDPSSLTGIFGVSPSTSLFWGLQVYQNSVVAI PSLIPVFN 425
 425 -----PTTSTPTTTPQATPTTTPQATPTT-----TPQATPTTTPQ 464
 426 LSPHKLAVTLGLASIAEIV---LGLPRPAIVSVVMPGCPGR VREG 471
 465 TTP--TPELTPPTTPEPTMPPTLEPTT-----PTSPTTLLHSRNTFLIGPEL 516
 472 EACCEAHTPPAVHSHNAP 490
 517 TSPCTTSEYPIVPSLVHLP 535

Search completed: September 17, 2002, 09:54:24
 Job time: 260 sec

